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Patentanmeldung Nr. Patent application No. Demande de brevet n°

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Protein complexes

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1. FIELD OF THE INVENTION

The present invention relates to protein complexes of the APP-processing pathway including the protein FADS2, component proteins thereof. The present invention also relates to methods for use of said complexes and in particular the use of FADS2 and also the proteins DEGS and SCD4 in, inter alia, in screening, diagnosis and therapy.

2. BACKGROUND OF THE INVENTION

Alzheimer's disease is a chronic condition that affects millions of individuals worldwide. After onset of the disease sufferers require a high degree of supervision and care. As the proportion of aged individuals in the population increases, the number of sufferers of Alzheimer's disease is expected to expand dramatically. Current top drugs (e.g. Aricept®/donepezil) attempt to achieve a temporary improvement of cognitive functions by inhibiting acetylcholinesterase, which results in increased levels of the neurotransmitter acetylcholine in the brain. These therapies are not suitable for later stages of the disease, they do not treat the underlying disease pathology, and they do not halt disease progression. The growing need for an effective therapy, coupled with the absence of effective treatments, presents a significant opportunity for drug target development and drug discovery.

The brains of sufferers of Alzheimer's disease show a characteristic pathology of prominent neuropathologic lesions, such as the initially intracellular neurofibrillary tangles (NFTs), and the extracellular amyloid-rich senile plaques. These lesions are associated with massive loss of populations of CNS neurons and their progression accompanies the clinical dementia associated with AD. The major component of amyloid plaques is the amyloid beta peptide. Amyloid beta is the proteolytic product of a precursor protein, beta amyloid precursor protein (beta-APP or APP). APP is a type-I trans-membrane protein which is cleaved by several different membrane-associated proteases. The first cleavage of APP occurs extracellularly by one of two proteases, alpha-secretase or beta-secretase. Beta-secretase or BACE1 (beta-site APP-cleaving enzyme) is a type-I transmembrane protein containing an aspartyl protease activity (described in detail below). Alpha secretase is a metalloprotease whose activity is most likely to be provided by one or a combination of the proteins ADAM10 and ADAM17. Following either the beta or alpha cleavage of APP, the final cleavage event occurs within the membrane and is

carried out by a protein complex called gamma secretase. It is the combination of the beta and gamma secretase activities that results in the liberation of the Abeta peptides of 40 and 42 residues (there are also lower levels of other forms) from the APP and ultimately the formation of the amyloid plaques responsible for the pathology of Alzheimer's disease. It is believed that the Abeta-42 peptide is the most critical Abeta species, because it shows the most pronounced neurotoxicity, and can aggregate easily, thus forming a nucleus for the aggregation of other Abeta peptides, such as the Abeta-40 which is typically produced at higher levels than the other species.

There is a strong need to develop novel therapies for the treatment of Alzheimer. However, so far the development of new therapies have been hampered by the incomplete understanding of the molecular processes. There has been a need to identify further proteins which could serve as targets for novel therapies.

3. SUMMARY OF THE INVENTION

An object of the present invention was to identify protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes and thus, to provide novel targets enabling novel therapies for the treatment of Alzheimer's disease.

Furthermore, it was an object to provide novel protein targets for the screening/development of novel therapies for the treatment of Alzheimer's disease

The present invention relates to protein complexes of APP processing pathway including the protein FADS2, component proteins thereof. The present invention also relates to methods for use of said complexes and in particular the use of FADS2 and also the proteins DEGS and SCD4 in, inter alia, screening, diagnosis and therapy of Alzheimer's disease and as screening tools for the identification of novel compounds for the treatment of Alzheimer's disease.

By applying the process according to the invention complexes associated with key proteins of the APP-pathway were identified. In particular, the protein complexes

associated with presenilin-2, Nicastrin, Bace1 and PTK7 were identified. The components are listed in table 1.

Presenilins

Presenilins 1 and 2 (PS1 and PS2) are integral membrane proteins which are localised in the endoplasmic reticulum, the Golgi and also at the cell surface [1]. They are predominantly found as a heterodimers of the NTF and CTF endoproteolytic fragments. The protease that cleaves presenilins (the "presenilinase") is not known, it is likely that the process is autocatalytic, also the functional significance of PS (auto)proteolysis is unclear.

Presenilins are involved in the proteolytical processing of Amyloid precursor protein (APP) [2] and the Notch receptor [3, 4]. In addition, Presenilins are associated with the cell-adhesion proteins alpha and beta-catenin, N-cadherin, and E-cadherin [5] [6] and other members of the armadillo family [7] [8] [9] [10].

APP processing by Presenilins is through their effects on gamma-secretase which cleaves APP, generating the C-terminus of the A-beta peptide. PS1 associates with the C83 and C99 processed C-terminal fragments of APP [11], Nicastrin [12] and Pen-2 [13]. Aph-1 [14] [13] is required in Presenilin processing. It is not clear whether Presenilins regulate gamma-secretase activity directly or whether they are protease enzymes themselves [15]. The gamma secretase activity could comprise a multimeric complex of these proteins [12] [16] but it is not known how the relationship between these proteins affects secretase activity.

Familial Alzheimer's disease (FAD) patients carry mutations in the presenilin proteins (PS1; PS2) or in APP. These mutations result in increased production of A-beta42 [17] which is the main component of cerebral plaques in FAD [18].

Understanding the composition of the gamma-secretase complex, the relationship between its component parts and its regulation are important in the design of drugs for use in Alzheimer's disease patients.

Nicastrin

Nicastrin is a type 1 trans-membrane glycoprotein with a conserved transmembrane domain and DYIGS motif [12] which is constitutively expressed in neural cell lines [19]. Biochemical studies have shown that Nicastrin binds to Presenilins 1 and 2, C-terminal derivatives of APP [12], membrane-tethered forms of Notch [20] and that it

is a member of the gamma-secretase complex along with PS1 and PS2 [16]. Gamma secretase activity is involved in the cleavage of both Notch and APP. It has been shown that Nicastrin is required for the intra-membrane cleavage of Notch [21] and APP [22], it may also have a role in post-translational stabilisation of Presenilin [23].

Aph-1 [14] and Pen-2 [13] were cloned recently in a screen for presenilin enhancers ("pen") in *C. elegans* and shown to interact genetically with Aph-2 (Nicastrin). Defects in Aph-1 affect Notch signalling and Nicastrin localisation [14]. Aph-1 and Pen-2 are required for Notch cleavage, gamma-secretase activity and the accumulation of processed Presenilins. Francis et al. [13] cloned the putative human orthologues of these genes, Aph-1a, Aph-1b and Pen-2, and recently Lee et al. [24] also cloned the human Aph-1 cDNAs.

The exact components of the gamma-secretase complex are not known but these two novel proteins could be components of or accessory factors to the complex and may interact together directly with Presenilin or with a Presenilin/Nicastrin complex. Nicastrin is therefore a member of the active gamma-secretase complex and there is recent evidence that it is the fully glycosylated form of the protein which is important in this complex. [25-29]

BACE1 (beta-secretase)

Vassar et al. [31] cloned a transmembrane aspartic protease that had the characteristics of the postulated beta-secretase of APP. Three other groups also cloned BACE1 using different approaches. BACE1 knockout mice have a normal phenotype, suggesting that therapeutic inhibition of BACE1 for AD may be free of mechanism-based toxicity. BACE1 ^{-/-} mice who are also homozygous for an amyloid precursor protein transgene lack brain beta-amyloid and beta-secretase-cleaved APP C-terminal fragments. [32]. Brain and primary cortical cultures from BACE1 knockout mice showed no detectable beta-secretase activity, and primary cortical cultures from BACE knockout mice produced much less amyloid-beta from APP. This suggests that BACE1, rather than its paralogue BACE2, is the main beta-secretase for APP.

BACE1 is a protein of 501 amino acids containing a 21-aa signal peptide followed by a proprotein domain spanning aa 22 to 45. There are alternatively spliced forms, BACE-I-457 and BACE-I-476. The luminal domain of the mature protein is followed by one predicted transmembrane domain and a short cytosolic C-terminal tail of 24 aa. BACE1 is predicted to be a type 1 transmembrane protein with the active site on the

luminal side of the membrane, where beta-secretase cleaves APP and possible other yet unidentified substrates. BACE1 mRNA in rat brain is present at higher levels in neurons than in glia, supporting that neurons are the primary source of the extracellular A-beta deposited in plaques. Sequence and mass spectrometry analyses showed that asn153, asn172, asn223, and asn354 of the BACE1 ectodomain are N-glycosylation sites. In addition, the ectodomain contains 6 cys residues that form disulfide bridges between positions 216 and 420, 278 and 443, and 330 and 380. The C-terminal domain of BACE1 contains a dileucine motif (LL499/500) that can potentially regulate its trafficking and endocytosis, and an adjacent serine, which is a casein kinase 1 phosphorylation site (S498) [33]. The propeptide is predominantly cleaved from BACE1 by furin [34]. In cells expressing wt or Swedish mutant APP, transient overexpression of BACE1 decreased alpha-secretase cleavage and increased beta-secretase activity at the known beta-secretase positions, asp1 and glu11. Although BACE1 is clearly a key enzyme required for the processing of APP into Ab, other potential substrates and functions of BACE1 are unknown. Also, no BACE1 interacting proteins with regulatory or modulatory functions have been described. Proteins that activate BACE1 activity would form suitable intervention points for Alzheimer's disease therapy. In addition, proteins that inhibit BACE1, like substrates or pseudosubstrates, could also provide suitable means of intervention e.g. as proteins therapeutics.

Protein Tyrosine Kinase 7 (PTK7)

PTK7, also referred to as colon carcinoma kinase 4 (CCK4), is an immunoglobulin superfamily transmembrane glycoprotein related to chicken KLG and *D. melanogaster* off-track. The gene has been mapped to human chromosome 6p21.1-->p12.2 by fluorescence in situ hybridization (Banga et al., 1997, Cytogenet Cell Genet. 1997;76(1-2):43-4).

PTK7, several splicing variants of which exist in human tissues, differs from the receptor tyrosine kinase consensus sequence in several positions, suggesting that the protein be catalytically inactive (Mossie et al., 1995, Oncogene. 1995 Nov 16;11(10):2179-84.).

PTK7 is expressed in multiple human tissues, but its function is unknown. However, its similarity to the *D. melanogaster* transmembrane protein Off-track/Dtrk, which serves as a coreceptor of plexin A for semaphorins Sema 1A (Winberg et al., Neuron. 2001 Oct 11;32(1):53-62) and Sema 6D (Toyofuku et al., Genes Dev. 2004 Feb 15;18(4):435-47.),

suggests that PTK7 might act as a coreceptor of a plexin-like protein. In the CNS, PTK7 might therefore play a role in maintenance of neuronal connectivity.

Said object is further achieved by the characterization of component proteins. These proteins are listed in table 2.

Furthermore, using functional assays, novel targets enabling novel therapies for the treatment of Alzheimer's disease were identified, namely FADS2, DEGS, SCD4

Fatty acid $\Delta 6$ desaturase (FADS2) has been known to catalyze the rate-limiting step in the biosynthesis of polyunsaturated fatty acids (PUFA), the conversion of either linoleic acid (C18:2) into γ -linolenic acid (gLA; C18:3n-6) in the n-6 metabolic pathway or of α -linolenic acid (aLA; C18:3n-3) into stearidonic acid (C18:4n-3) in the n-3 metabolic pathway. gLA is subsequently elongated and converted to arachidonic acid (AA; C20:4n-6) by fatty acid $\Delta 5$ desaturase (FADS1). AA is the essential precursor of various eicosanoids, such as prostaglandins and leukotrienes. In the n-3 metabolic pathway, FADS1 generates eicosapentaenoic acid (EPA; C20:5n-3), a PUFA that has been suggested to have neuroprotective effects (Lynch et al., 2003) and to be beneficial in the treatment of schizophrenia and depression (Emsley et al., 2003).

Another elongation step converts EPA into docosapentaenoic acid (DPA; C22:5n-3) and further to C24:5n-3. This PUFA and the analogous n-6 fatty acid, C24:4n-6, are additional substrates of FADS2, which converts them into C24:6n-3 and C24:5n-6, respectively. Both C24 PUFAs are partially oxidized in peroxisomes to give rise to docosahexaenoic acid (DHA; C22:6n-3), a major brain PUFA, and C22:5n-6, respectively.

Three human FADS family members have been cloned (see also for rodents (Cho et al (1999), J Biol Chem 274, 37335-37339; Marquardt, A (2000) Genomics 66, 175). All are fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both characterized by conserved His-motifs. FADS genes are clustered at 11q12-q13.1; likely arisen from gene duplication. The function of a related gene product, FADS3, is unknown, but given the high level of sequence similarity between FADS2 and FADS3 it has been proposed that FADS3 may constitute an alternative fatty acid $\Delta 6$ desaturase.

According to the functional assays provided herein, $\Delta 5$ desaturase (FADS1) does not have an effect on the metabolism of APP.

Thus FADS1 (SEQ ID 122) and the orthologs thereof are excluded from the scope of the invention. Those sequences are thus excluded from the general definition of homologs provided herein.

FADS3 (SEQ ID 125), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity

is explicitly included within the scope of the invention as a screening tool for compounds for the treatment of Alzheimer's disease and/or the modulation of gamma-secretase-activity

Thus, the invention relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant

of said second protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;
 and a complex (II) comprising at least two of said second proteins,
 wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. A protein complex comprising a first protein selected from the proteins listed in table 1, second column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
3. A protein complex comprising the proteins selected from the proteins in table 1, third column or a homologue thereof, or a variant thereof or functionally active fragments or functionally active derivatives of said proteins, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, but 1 to the number of proteins listed in table 1, fifth column of said complex, or a homologue or a variant thereof, or a functionally active fragment or functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins of said fifth column under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
5. The complex of any of No. 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the biochemical activity as stated in table 3.
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:
Expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of No. 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

14. Nucleic acid encoding a protein according to No. 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to No.14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to No.1 (a) and at least one of said proteins, being selected from the second group of proteins according to No.1 (b).
16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and /or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid encoding at least one protein selected from the first group of proteins according to No.1 (a) and the nucleic acid encoding at least one protein selected from the second group of proteins according to No.1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, which binds the complex of any of No.1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and/or an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the group of proteins according to No. 13.
18. A kit comprising in one or more containers the complex of any of No. 1 - 8 and/or the proteins of No. 13, optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.
19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
21. Array in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for processing a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the proteins according to No. 13.
24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
25. A method for screening for a molecule that binds to the complex of any one of No. 1 - 8 and/or any of the proteins of No.13, comprising the following steps:
 - (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:
 - (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex

dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.
29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.
31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as

neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.
36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a

substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex are determined.
40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody of fragment of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or any of the proteins listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

In particular, the invention relates to FADS2 or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity, with the proviso that FADS1 (SEQ 122) is excluded.

Furthermore, the invention relates to DEGS (SEQ ID 123) and SCD4 (SEQ ID 123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity

3.1 DEFINITIONS

The term "activity" as used herein, refers to the function of a molecule in its broadest sense. It generally includes, but is not limited to, biological, biochemical, physical or chemical functions of the molecule. It includes for example the enzymatic activity, the ability to interact with other molecules and ability to activate, facilitate, stabilize, inhibit, suppress or destabilize the function of other molecules, stability, ability

to localize to certain subcellular locations. Where applicable, said term also relates to the function of a protein complex in its broadest sense.

The term "agonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, increases the amount of, or prolongs the duration of, the activity of the complex. The stimulation may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Agonists may include proteins, nucleic acids, carbohydrates or any other organic or inorganic molecule or metals. Agonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred activators are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 25%, at least 50%, at least 100%, at least, 200%, at least 500% or at least 1000% at a concentration of the activator $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} . Any combination of the above mentioned degrees of percentages and concentration may be used to define an agonist of the invention, with greater effect at lower concentrations being preferred.

The term "amount" as used herein and as applicable to the embodiment described relates to the amount of the particular protein or protein complex described, including the value of null, i.e. where no protein or protein complex described in that particular embodiment is present under the or any of the conditions which might be specified in that particular embodiment.

The term "animal" as used herein includes, but is not limited to mammals, preferably mammals such as cows, pigs, horses, mice, rats, cats, dogs, sheep, goats and most preferably humans. Other animals used in agriculture, such as chickens, ducks etc. are also included in the definition as used herein.

The term "animal" as used herein does not include humans if being used in the context of genetic alterations to the germline.

The term "antagonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, decreases the amount of, or the duration

or level of activity of the complex. The effect may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Antagonists may include proteins, including antibodies, nucleic acids, carbohydrates or any other organic or inorganic molecule or metals. Antagonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred antagonists are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplarily illustrated above by at least 10%, at least 20%, at least 30%, at least 40% at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or at least 99% at a concentration of the inhibitor of $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} .

Any combination of the above mentioned degrees of percentages and concentration may be used to define antagonist of the invention, with greater effect at lower concentrations being preferred.

The term "antibodies" as used herein, include include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library.

The term "binding" as used herein means a stable or transient association between two molecules, including electrostatic, hydrophobic, ionic and/or hydrogen-bond interaction under physiological conditions and/or conditions being used in diagnostic or prognostic method or process or procedure.

The term "carrier" as used herein refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc,

sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

If not stated otherwise, the terms "complex" and "protein complex" are used interchangeably herein and refer to a complex of proteins that is able to perform one or more functions of the wild type protein complex. The protein complex may or may not include and/or be associated with other molecules such as nucleic acid, such as RNA or DNA, or lipids or further cofactors or moieties selected from a metal ions, hormones, second messengers, phosphate, sugars.

A "complex" of the invention may also be part of or a unit of a larger physiological protein assembly.

If not stated otherwise, the term "compound" as used herein are include but are not limited to peptides, nucleic acids, carbohydrates, natural product extract librariesorganic molecules, preferentially small organic molecules, anorganic molecules, including but not limited to chemicals, metals and organometallic molecules.

The terms "derivatives" or "analogs of component proteins" or "variants" as used herein include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions. It means a protein which is the outcome of a modification of the naturally occurring protein, by amino acid substitutions, deletions

and additios, respectively, which derivatives still exhibit the biological function of the naturally occurring protein although not necessarily to the same degree. The biological function of such proteins can e.g. be examined by suitable available in vitro assays as provided in the invention.

The term "functionally active" as used herein refers to a polypeptide, namely a fragment or derivative, having structural, regulatory, or biochemical functions of the protein according to the embodiment of which this polypeptide, namely fragment or derivative is related to.

The term "fragment" as used herein refers to a polypeptide of at least 10, 20, 30, 40 or 50 amino acids of the component protein according to the embodiment. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids.

The term "gene" as used herein refers to a nucleic acid comprising an open reading frame encoding a polypeptide of, if not stated otherwise, the present invention, including both exon and optionally intron sequences.

The terms "homologue" or "homologous gene products" as used herein mean a protein in another species, preferably mammals, which performs the same biological function as the a protein component of the complex further described herein. Such homologues are also termed "orthologous gene products". The algorithm for the detection of orthologue gene pairs from humans and mammals or other species uses the whole genome of these organisms. First, pairwise best hits are retrieved, using a full Smith-Waterman alignment of predicted proteins. To further improve reliability, these pairs are clustered with pairwise best hits involving *Drosophila melanogaster* and *C. elegans* proteins. Such analysis is given, e.g., in Nature, 2001, 409:860-921. The homologues of the proteins according to the invention can either be isolated based on the sequence homology of the genes encoding the proteins provided herein to the genes of other species by cloning the respective gene applying conventional technology and expressing the protein from such gene, or by isolating proteins of the other species by isolating the analogous complex according to the methods provided herein or to other suitable methods commonly known in the art.

The term "host cells" or, where applicable, "cells" or "hosts" as used herein is intended to be understood in a broadest sense and include, but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid

DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

It is understood that this term not only refers to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

As used herein, the term "modulation of γ -secretase activity" refers to an effect on the processing of APP by the gamma-secretase-complex. Preferably it refers to an effect in which the overall rate of processing of APP remains essentially as without the application of said compounds, but in which the relative quantities of the processed products are changed, more preferably in such a way that the amount of the A β 42-peptide produced is reduced.

The term "nucleic acid" as used herein refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to polynucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the in vivo activity or lifespan of polynucleotides of the invention. Polynucleotides according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques. The polynucleotides are typically provided in isolated and/or purified form. As applicable to the embodiment being described, they include both single stranded and double-stranded polynucleotides.

The term "percent identity", as used herein, means the number of identical residues as defined by an optimal alignment using the Smith-Waterman algorithm divided by the length of the overlap multiplied by 100. The alignment is performed by the search program (Pearson, 1991, Genomics 11:635-650) with the constraint to align the maximum of both sequences.

The terms "polypeptides" and "proteins" are, where applicable, used interchangeably herein. They may be chemically modified, e.g. post-translationally modified. For example, they may be glycosylated or comprise modified amino acid residues. They may also be modified by the addition of a signal sequence to promote their secretion from a cell where the polypeptide does not naturally contain such a sequence. They may be tagged with a tag. They may be tagged with different labels which may assist in identification of the proteins in a protein complex. Polypeptides/proteins for use in the invention may be in a substantially isolated form. It will be understood that the polypeptid/protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the polypeptide and still be regarded as substantially isolated. A polypeptide/protein for use in the invention may also be in a substantially purified form, in which case it will generally comprise the polypeptide in a preparation in which more than 50%, e.g. more than 80%, 90%, 95% or 99%, by weight of the polypeptide in the preparation is a polypeptide of the invention.

"Target for therapeutic drug" means that the respective protein (target) can bind the active ingredient of a pharmaceutical composition and thereby changes its biological activity in response to the drug binding.

The term "tag" as used herein is meant to be understood in its broadest sense and to include, but is not limited to any suitable enzymatic, fluorescent, or radioactive labels and suitable epitopes, including but not limited to HA-tag, Myc-tag, T7, His-tag, FLAG-tag, Calmodulin binding proteins, glutathione-S-transferase, strep-tag, KT3-epitope, EEF-epitopes, green-fluorescent protein and variants thereof.

The term "therapeutics" as used herein, includes, but is not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments); antibodies thereto; nucleic acids encoding the component protein, and analogs or derivatives thereof; component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The term "vector" as used herein means a nucleic acid molecule capable of transporting another nucleic acid sequence to which it has been linked. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. The terms "plasmid" and "vector" are used interchangeably herein when applicable to the embodiment. However, vectors other than plasmids are also included herein. The expression elements of vectors vary in their strengths and specificities.

Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

4. DETAILED DESCRIPTION OF THE INVENTION

Overview:

An object of the present invention was to identify protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes.

Furthermore, it was an object to provide novel protein targets for the screening/development of novel therapies for the treatment of Alzheimer's disease

The present invention relates to the protein complexes including the protein FADS2, component proteins thereof. The present invention also relates to methods for use of said complexes and in particular the use of FADS2 and also the proteins DEGS and SCD4 in, inter alia, screening, diagnosis and therapy.

By applying the process according to the invention said protein complex were identified. The components are listed in table 1.

Said object is further achieved by the characterisation of component proteins. These proteins are listed in table 2.

The invention thus relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said complex, or a functionally active derivative

thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

and a complex (II) comprising at least two of said second proteins,

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. A protein complex comprising a first protein selected from the proteins listed in table 1, second column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
3. A protein complex comprising the proteins selected from the proteins in table 1, third column or a homologue thereof, or a variant thereof or functionally active fragments or functionally active derivatives of said proteins, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, but 1 to the number of proteins listed in table 1, fifth column of said complex, or a homologue or a variant thereof, or a functionally active fragment or functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins of said fifth column under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
5. The complex of any of No. 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the biochemical activity as stated in table 3.
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:
Expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of No. 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

14. Nucleic acid encoding a protein according to No. 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to No.14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to No.1 (a) and at least one of said proteins, being selected from the second group of proteins according to No.1 (b).
16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and /or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid encoding at least one protein selected from the first group of proteins according to No.1 (a) and the nucleic acid encoding at least one protein selected from the second group of proteins according to No.1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, which binds the complex of any of No.1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and/or an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the group of proteins according to No. 13.
18. A kit comprising in one or more containers the complex of any of No. 1 - 8 and/or the proteins of No. 13, optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.
19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.
20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

21. Array in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for processing a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the proteins according to No. 13.
24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
25. A method for screening for a molecule that binds to the complex of any one of No. 1 - 8 and/or any of the proteins of No.13, comprising the following steps:
(a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
(b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:
(a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
(b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular

localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.
29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.
31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of

a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.
36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of No. 35, wherein the amount of the individual protein components of said complex are determined.

40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody of fragment of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or any of the proteins listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the invention relates to DEGS (SEQ ID 123) and SCD4 (SEQ ID 123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM

EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity

Animal models are also provided herein.

Preferably, the protein components of the complexes described herein are all mammalian proteins. The complexes can also consist only of the respective homologues from other mammals such as mouse, rat, pig, cow, dog, monkey, sheep or horse or other species such as *D. melanogaster*, *C. elegans* or chicken. In another preferred embodiment, the complexes are a mixture of proteins from two or more species.

TABLES:

Table 1: Composition of Complexes

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Entry point'): Lists the bait proteins that have been chosen for the purification of the given complex.

Third column ('All interactors'): Lists all novel interactors which have been identified as members of the complex and all interactors which have been known to be associated with the bait so far.

Fourth column ('Known interactors'): Lists all interactors which have been known to be associated with the bait so far.

Fifth column ('Novel interactors of the complex'): Lists all novel interactors of the complex which have been identified in the experiments provided herein.

Sixth column: Separately lists the members of the newly identified complex which have not been annotated previously.

Table 2: Individual Proteins of the Complexes

First column ('Protein'): Lists in alphabetical order all proteins which have been identified as interactors of the complexes presented herein.

Second column ('SEQ ID'): Lists the SEQ ID (Sequence Identifications) of the proteins herein as used herein.

Third column ('IPI-Numbers'): Lists the IPI-Numbers of the proteins herein. The IPI-Numbers refer to the International Protein Index created by the European Bioinformatics Institute (EMBL-EBI), Hinxton, UK.

Fourth column ('Molecular Weight'): Lists the Molecular Weight of the proteins in Dalton.

Table 3: Biochemical Activities of the Complexes of the invention.

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Biochemical Activity'): Lists biochemical activities of the complexes. Assays in order to test these activities are also provided herein (infra).

FIGURES

Figure 1: Schematic representation of FADS2-containing protein complexes. FADS2 is a component of BACE1-, Nicastrin- and PTK7- protein complexes.

TAP-tagged BACE1, Nicastrin and PTK7 were retrovirally transduced into SKNBE2 neuroblastoma cells and the respective protein complexes were subsequently obtained by tandem-affinity purification. Associated proteins were identified by liquid chromatography-MS/MS.

Figure 2:

FADS2 is highly expressed in human brain.

FADS2-specific primers and equal amounts of total RNA from various human tissue sources were utilized for determination of relative expression levels of FADS2 by quantitative PCR. Three independent experiments were performed and all values were normalized to a human reference RNA (Universal Human Reference RNA, Stratagene, No. 740000).

Figure 3 A+B:

siRNA-mediated knock-down of FADS2 expression attenuates secretion of A β 1-42 from two different cell lines.

(upper panels) siRNAs directed against BACE1, FADS2 (A and B) or Luc3 were transfected into SKNBE2 neuroblastoma cells (FIGURE 3 A) or H4 neuroglioma cells (FIGURE 3 B) over-expressing mutant APP^{sw}. 48h after transfection growth medium

was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(lower panels) siRNAs directed against FADS2 (A and B) or Luc3 were co-transfected with CTAP-FADS2 into SKNBE2 neuroblastoma cells (Figure 3 A) or H4 neuroglioma cells (Figure 3 B). 48h after transfection cells were lysed. 30 μ g of the lysates were separated by SDS-PAGE, transferred to nitrocellulose and probed with antibodies directed either against the TAP-tag or against tubulin.

Figure 4:

SCD4 is very highly expressed in human brain.

5 μ g of total RNA from various human tissue sources (Clontech) was reverse transcribed. Equal amounts of that cDNA and SCD4-specific primers were utilized for determination of relative expression levels of SCD4 by quantitative PCR. Three independent experiments were performed and all values were normalized to a human reference RNA (Stratagene).

Figure 5:

siRNA-mediated knock-down of SCD4 expression attenuates secretion of A β 1-42.

(left panel) siRNAs directed against BACE1, SCD4 or Luc3 were transfected into H4 neuroglioma cells over-expressing mutant APPsw. 48h after transfection growth medium was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(right panel) siRNA directed against SCD4 specifically reduces mRNA levels. Total RNA was prepared from H4/APPsw cells transfected with siRNA directed against either Luc3 or SCD4. After reverse transcription, relative amounts of SCD4 transcripts were determined by quantitative PCR. At least two independent experiments were performed.

Figure 6:

DEGS is highly expressed in human brain.

5 μ g of total RNA from various human tissue sources (Clontech) was reverse transcribed. Equal amounts of that cDNA and DEGS-specific primers were utilized for determination of relative expression levels of DEGS by quantitative PCR. Three

independent experiments were performed and all values were normalized to a human reference RNA (Stratagene).

Figure 7:

siRNA-mediated knock-down of DEGS expression attenuates secretion of A β 1-42.

(left panel) siRNAs directed against BACE1, DEGS or Luc3 were transfected into H4 neuroglioma cells over-expressing mutant APPsw. 48h after transfection growth medium was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(right panel) siRNA directed against DEGS specifically reduces mRNA levels. Total RNA was prepared from H4/APPsw cells transfected with siRNA directed against either Luc3 or DEGS. After reverse transcription, relative amounts of DEGS transcripts were determined by quantitative PCR. At least two independent experiments were performed.

4.1 PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The protein complexes of the present invention and their component proteins are described in the Tables 1 - 3. The protein complexes and component proteins can be obtained by methods well known in the art for protein purification and recombinant protein expression. For example, the protein complexes of the present invention can be isolated using the TAP method described in Section 5, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety. Additionally, the protein complexes can be isolated by immunoprecipitation of the component proteins and combining the immunoprecipitated proteins. The protein complexes can also be produced by recombinantly expressing the component proteins and combining the expressed proteins.

The nucleic and amino acid sequences of the component proteins of the protein complexes of the present invention are provided herein (SEQ ID NO 1 - 121) (see. Furthermore sequences of the proteins DEGS and SCD4 are provided herein (SEQ ID 123 and 124 respectively), and can be obtained by any method known in the art, e.g., by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of each

sequence, and/or by cloning from a cDNA or genomic library using an oligonucleotide specific for each nucleotide sequence.

Homologues (e.g., nucleic acids encoding component proteins from other species) or other related sequences (e.g., variants, paralogs) which are members of a native cellular protein complex can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular nucleic acid sequence as a probe, using methods well known in the art for nucleic acid hybridization and cloning.

Exemplary moderately stringent hybridization conditions are as follows: prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μ g/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 μ g/ml denatured salmon sperm DNA and 5-20 $\times 10^6$ cpm of 32 P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50 °C for 45 min before autoradiography. Alternatively, exemplary conditions of high stringency are as follows: e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3). Other conditions of high stringency which may be used are well known in the art. Exemplary low stringency hybridization conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 μ g/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

For recombinant expression of one or more of the proteins, the nucleic acid containing all or a portion of the nucleotide sequence encoding the protein can be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted protein coding sequence. The necessary transcriptional and translational signals can also be supplied by the native promoter of the component protein gene, and/or flanking regions.

A variety of host-vector systems may be utilized to express the protein coding sequence. These include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

In a preferred embodiment, a complex of the present invention is obtained by expressing the entire coding sequences of the component proteins in the same cell, either under the control of the same promoter or separate promoters. In yet another embodiment, a derivative, fragment or homologue of a component protein is recombinantly expressed. Preferably the derivative, fragment or homologue of the protein forms a complex with the other components of the complex, and more preferably forms a complex that binds to an anti-complex antibody. Such an antibody is further described infra.

Any method available in the art can be used for the insertion of DNA fragments into a vector to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and protein coding sequences. These methods may include in vitro recombinant DNA and synthetic techniques and in vivo recombinant techniques (genetic recombination). Expression of nucleic acid sequences encoding a component protein, or a derivative, fragment or homologue thereof, may be regulated by a second nucleic acid sequence so that the gene or fragment thereof is expressed in a host transformed with the recombinant DNA molecule(s). For example, expression of the proteins may be controlled by any promoter/enhancer known in the art. In a specific embodiment, the promoter is not native to the gene for the component protein. Promoters that may be used can be selected from among the many known in the art, and are chosen so as to be operative in the selected host cell.

In a specific embodiment, a vector is used that comprises a promoter operably linked to nucleic acid sequences encoding a component protein, or a fragment, derivative or homologue thereof, one or more origins of replication, and optionally, one or more selectable markers (e.g., an antibiotic resistance gene).

In another specific embodiment, an expression vector containing the coding sequence, or a portion thereof, of a component protein, either together or separately, is made by subcloning the gene sequences into the EcoRI restriction site of each of the three pGEX vectors (glutathione S-transferase expression vectors; Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of products in the correct reading frame.

Expression vectors containing the sequences of interest can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene function, and (c) expression of the inserted sequences. In the first approach, coding sequences can be detected by nucleic acid hybridization to probes comprising sequences homologous and complementary to the inserted sequences. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" functions (e.g., resistance to antibiotics, occlusion body formation in baculovirus, etc.) caused by insertion of the sequences of interest in the vector. For example, if a component protein gene, or portion thereof, is inserted within the marker gene sequence of the vector, recombinants containing the encoded protein or portion will be identified by the absence of the marker gene function (e.g., loss of β -galactosidase activity). In the third approach, recombinant expression vectors can be identified by assaying for the component protein expressed by the recombinant vector. Such assays can be based, for example, on the physical or functional properties of the interacting species in in vitro assay systems, e.g., formation of a complex comprising the protein or binding to an anti-complex antibody.

Once recombinant component protein molecules are identified and the complexes or individual proteins isolated, several methods known in the art can be used to propagate them. Using a suitable host system and growth conditions, recombinant expression vectors can be propagated and amplified in quantity. As previously described, the expression vectors or derivatives which can be used include, but are not limited to, human or animal viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus, yeast vectors; bacteriophage vectors such as lambda phage; and plasmid and cosmid vectors.

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies or processes the expressed proteins in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically-engineered component proteins may

be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation, etc.) of proteins. Appropriate cell lines or host systems can be chosen to ensure that the desired modification and processing of the foreign protein is achieved. For example, expression in a bacterial system can be used to produce an unglycosylated core protein, while expression in mammalian cells ensures "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

In other specific embodiments, a component protein or a fragment, homologue or derivative thereof, may be expressed as fusion or chimeric protein product comprising the protein, fragment, homologue, or derivative joined via a peptide bond to a heterologous protein sequence of a different protein. Such chimeric products can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acids to each other by methods known in the art, in the proper coding frame, and expressing the chimeric products in a suitable host by methods commonly known in the art. Alternatively, such a chimeric product can be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Chimeric genes comprising a portion of a component protein fused to any heterologous protein-encoding sequences may be constructed.

In particular, protein component derivatives can be made by altering their sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA sequences that encode substantially the same amino acid sequence as a component gene or cDNA can be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of the component protein gene that are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. Likewise, the derivatives of the invention include, but are not limited to, those containing, as a primary amino acid sequence, all or part of the amino acid sequence of a component protein, including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity that acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the

sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

In a specific embodiment, up to 1%, 2%, 5%, 10%, 15% or 20% of the total number of amino acids in the wild type protein are substituted or deleted; or 1, 2, 3, 4, 5, or 6 or up to 10 or up to 20 amino acids are inserted, substituted or deleted relative to the wild type protein.

In a specific embodiment of the invention, the nucleic acids encoding a protein component and protein components consisting of or comprising a fragment of or consisting of at least 6 (continuous) amino acids of the protein are provided. In other embodiments, the fragment consists of at least 10, 20, 30, 40, or 50 amino acids of the component protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Derivatives or analogs of component proteins include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions.

In a specific embodiment, proteins are provided herein, which share an identical region of 20, 30, 40, 50 or 60 contiguous amino acids of the proteins listed in table 2.

The protein component derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, the cloned gene sequences can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The sequences can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated in vitro. In the production of the gene encoding a derivative,

homologue or analog of a component protein, care should be taken to ensure that the modified gene retains the original translational reading frame, uninterrupted by translational stop signals, in the gene region where the desired activity is encoded.

Additionally, the encoding nucleic acid sequence can be mutated in vitro or in vivo, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further in vitro modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis and in vitro site-directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551-6558), amplification with PCR primers containing a mutation, etc.

Once a recombinant cell expressing a component protein, or fragment or derivative thereof, is identified, the individual gene product or complex can be isolated and analyzed. This is achieved by assays based on the physical and/or functional properties of the protein or complex, including, but not limited to, radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled product, etc.

The component proteins and complexes may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the complexes or proteins), including but not restricted to column chromatography (e.g., ion exchange, affinity, gel exclusion, reversed-phase high pressure, fast protein liquid, etc.), differential centrifugation, differential solubility, or by any other standard technique used for the purification of proteins. Functional properties may be evaluated using any suitable assay known in the art.

Alternatively, once a component protein or its derivative, is identified, the amino acid sequence of the protein can be deduced from the nucleic acid sequence of the chimeric gene from which it was encoded. As a result, the protein or its derivative can be synthesized by standard chemical methods known in the art (e.g., Hunkapiller et al., 1984, Nature 310:105-111).

Manipulations of component protein sequences may be made at the protein level. Included within the scope of the invention is a complex in which the component proteins or derivatives and analogs that are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by

known techniques, including but not limited to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 , acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

In specific embodiments, the amino acid sequences are modified to include a fluorescent label. In another specific embodiment, the protein sequences are modified to have a heterofunctional reagent; such heterofunctional reagents can be used to crosslink the members of the complex.

In addition, complexes of analogs and derivatives of component proteins can be chemically synthesized. For example, a peptide corresponding to a portion of a component protein, which comprises the desired domain or mediates the desired activity in vitro (e.g., complex formation) can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the protein sequence.

In cases where natural products are suspected of being mutant or are isolated from new species, the amino acid sequence of a component protein isolated from the natural source, as well as those expressed in vitro, or from synthesized expression vectors in vivo or in vitro, can be determined from analysis of the DNA sequence, or alternatively, by direct sequencing of the isolated protein. Such analysis can be performed by manual sequencing or through use of an automated amino acid sequenator.

The complexes can also be analyzed by hydrophilicity analysis (Hopp and Woods, 1981, *Proc. Natl. Acad. Sci. USA* 78:3824-3828). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the proteins, and help predict their orientation in designing substrates for experimental manipulation, such as in binding experiments, antibody synthesis, etc. Secondary structural analysis can also be done to identify regions of the component proteins, or their derivatives, that assume specific structures (Chou and Fasman, 1974, *Biochemistry* 13:222-23). Manipulation, translation, secondary structure prediction, hydrophilicity and hydrophobicity profile predictions, open reading frame prediction and plotting, and determination of sequence homologies, etc., can be accomplished using computer software programs available in the art.

Other methods of structural analysis including but not limited to X-ray crystallography (Engstrom, 1974, *Biochem. Exp. Biol.* 11:7-13), mass spectroscopy and gas chromatography (Methods in Protein Science, J. Wiley and Sons, New York, 1997), and computer modeling (Fletterick and Zoller, eds., 1986, *Computer Graphics and*

Molecular Modeling, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, New York) can also be employed.

4.2 ANTIBODIES TO PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

According to the present invention, a protein complex of the present invention comprising a first protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in third column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, can be used as an immunogen to generate antibodies which immunospecifically bind such immunogen. According to the present invention, also a protein complex of the present invention can be used as an immunogen to generate antibodies which immunospecifically bind to such immunogen comprising all proteins listed in fifth column of table 1.

Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. In a specific embodiment, antibodies to a complex comprising human protein components are produced. In another embodiment, a complex formed from a fragment of said first protein and a fragment of said second protein, which fragments contain the protein domain that interacts with the other member of the complex, are used as an immunogen for antibody production. In a preferred embodiment, the antibody specific for the complex in that the antibody does not bind the individual protein components of the complex.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression

of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected for (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those on the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor et al., 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* 1994, Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the

hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al., 1991, *Bio/Technology* 9:1370-1372; Hay et al., 1992, *Hum. Antibod. Hybridomas* 3:81-85; Huse et al., 1989, *Science* 246:1275-1281; Griffiths et al., 1993, *EMBO J.* 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al., 1988, *Science* 240:1041-1043; Liu et al., 1987, *Proc. Natl. Acad.*

Sci. USA 84:3439-3443; Liu et al., 1987, J. Immunol. 139:3521-3526; Sun et al., 1987, Proc. Natl. Acad. Sci. USA 84:214-218; Nishimura et al., 1987, Canc. Res. 47:999-1005; Wood et al., 1985, Nature 314:446-449; and Shaw et al., 1988, J. Natl. Cancer Inst. 80:1553-1559); Morrison, 1985, Science 229:1202-1207; Oi et al., 1986, Bio/Techniques 4:214; U.S. Patent 5,225,539; Jones et al., 1986, Nature 321:552-525; Verhoeyan et al., 1988, Science 239:1534; and Beidler et al., 1988, J. Immunol. 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., 1994, Bio/technology 12:899-903).

Antibody fragments that contain the idiotypes of the complex can be generated by techniques known in the art. For example, such fragments include, but are not limited to, the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragment that can be generated by reducing the disulfide bridges of

the F(ab')₂ fragment; the Fab fragment that can be generated by treating the antibody molecular with papain and a reducing agent; and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a particular domain of the complex, or a derivative thereof, one may assay generated hybridomas for a product that binds to the fragment of the complex, or a derivative thereof, that contains such a domain. For selection of an antibody that specifically binds a complex of the present, or a derivative, or homologue thereof, but which does not specifically bind to the individual proteins of the complex, or a derivative, or homologue thereof, one can select on the basis of positive binding to the complex and a lack of binding to the individual protein components.

Antibodies specific to a domain of the complex, or a derivative, or homologue thereof, are also provided.

The foregoing antibodies can be used in methods known in the art relating to the localization and/or quantification of the complexes of the invention, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples (by immunoassay), in diagnostic methods, etc. This hold true also for a derivative, or homologue thereof of a complex.

In another embodiment of the invention (see *infra*), an antibody to a complex or a fragment of such antibodies containing the antibody binding domain, is a therapeutic.

4.3 DIAGNOSTIC, PROGNOSTIC, AND SCREENING USES OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The particular protein complexes and proteins of the present invention may be markers of normal physiological processes, and thus have diagnostic utility. Further, definition of particular groups of patients with elevations or deficiencies of a protein complex of the present invention, or wherein the protein complex has a change in protein component composition, can lead to new nosological classifications of diseases, furthering diagnostic ability.

Examples for diseases or disorders are neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Detecting levels of protein complexes, or individual component proteins that form the complexes, or detecting levels of the mRNAs encoding the components of the complex, may be used in diagnosis, prognosis, and/or staging to follow the course of a disease state, to follow a therapeutic response, etc.

A protein complex of the present invention and the individual components of the complex and a derivative, analog or subsequence thereof, encoding nucleic acids (and sequences complementary thereto), and anti-complex antibodies and antibodies directed against individual components that can form the complex, are useful in diagnostics. The foregoing molecules can be used in assays, such as immunoassays, to detect, prognose, diagnose, or monitor various conditions, diseases, and disorders characterized by aberrant levels of a complex or aberrant component composition of a complex, or monitor the treatment of such various conditions, diseases, and disorders.

In particular, such an immunoassay is carried out by a method comprising contacting a sample derived from a patient with an anti-complex antibody under conditions such that immunospecific binding can occur, and detecting or measuring the amount of any immunospecific binding by the antibody. In a specific aspect, such binding of antibody, in tissue sections, can be used to detect aberrant complex localization, or aberrant (e.g., high, low or absent) levels of a protein complex or complexes. In a specific embodiment, an antibody to the complex can be used to assay a patient tissue or serum sample for the presence of the complex, where an aberrant level of the complex is an indication of a diseased condition. By "aberrant levels" is meant increased or decreased levels relative to that present, or a standard level representing that present, in an analogous sample from a portion or fluid of the body, or from a subject not having the disorder.

The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few known in the art.

Nucleic acids encoding the components of the protein complex and related nucleic acid sequences and subsequences, including complementary sequences, can be used in hybridization assays. The nucleic acid sequences, or subsequences thereof,

comprising about at least 8 nucleotides, can be used as hybridization probes. Hybridization assays can be used to detect, prognose, diagnose, or monitor conditions, disorders, or disease states associated with aberrant levels of the mRNAs encoding the components of a complex as described, supra. In particular, such a hybridization assay is carried out by a method comprising contacting a sample containing nucleic acid with a nucleic acid probe capable of hybridizing to component protein coding DNA or RNA, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

In specific embodiments, diseases and disorders involving or characterized by aberrant levels of a protein complex or aberrant complex composition can be diagnosed, or its suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by determining the component protein composition of the complex, or detecting aberrant levels of a member of the complex or un-complexed component proteins or encoding nucleic acids, or functional activity including, but not restricted to, binding to an interacting partner, or by detecting mutations in component protein RNA, DNA or protein (e.g., mutations such as translocations, truncations, changes in nucleotide or amino acid sequence relative to wild-type that cause increased or decreased expression or activity of a complex, and/or component protein.

Such diseases and disorders include, but are not limited to neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

By way of example, levels of a protein complex and the individual components of a complex can be detected by immunoassay, levels of component protein RNA or DNA can be detected by hybridization assays (e.g., Northern blots, dot blots, RNase protection assays), and binding of component proteins to each other (e.g., complex formation) can be measured by binding assays commonly known in the art. Translocations and point mutations in component protein genes can be detected by Southern blotting, RFLP analysis, PCR using primers that preferably generate a fragment spanning at least most of the gene by sequencing of genomic DNA or cDNA obtained from the patient, etc.

Assays well known in the art (e.g., assays described above such as immunoassays, nucleic acid hybridization assays, activity assays, etc.) can be used to determine whether one or more particular protein complexes are present at either increased or decreased levels, or are absent, in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or

disorder, as compared to the levels in samples from subjects not having such a disease or disorder, or having a predisposition to develop such a disease or disorder. Additionally, these assays can be used to determine whether the ratio of the complex to the un-complexed components of the complex, is increased or decreased in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the ratio in samples from subjects not having such a disease or disorder.

In the event that levels of one or more particular protein complexes (i.e., complexes formed from component protein derivatives, homologs, fragments, or analogs) are determined to be increased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder, or predisposition for a disease or disorder, can be diagnosed, have prognosis defined for, be screened for, or be monitored by detecting increased levels of the one or more protein complexes, increased levels of the mRNA that encodes one or more members of the one or more particular protein complexes, or by detecting increased complex functional activity.

Accordingly, in a specific embodiment of the present invention, diseases and disorders involving increased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting increased levels of the one or more protein complexes, the mRNA encoding both members of the complex, or complex functional activity, or by detecting mutations in the component proteins that stabilize or enhance complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that stabilize or enhance complex formation.

In the event that levels of one or more particular protein complexes are determined to be decreased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder or predisposition for a disease or disorder can be diagnosed, have its prognosis determined, be screened for, or be monitored by detecting decreased levels of the one or more protein complexes, the mRNA that encodes one or more members of the particular one or more protein complexes, or by detecting decreased protein complex functional activity.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving decreased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting decreased levels of the one or more protein complexes, the mRNA encoding one or more members of the one or more complexes, or complex functional activity, or by detecting mutations in the component proteins that decrease complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that decrease complex formation.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving aberrant compositions of the complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting the component proteins of one or more complexes, or the mRNA encoding the members of the one or more complexes.

The use of detection techniques, especially those involving antibodies against a protein complex, provides a method of detecting specific cells that express the complex or component proteins. Using such assays, specific cell types can be defined in which one or more particular protein complexes are expressed, and the presence of the complex or component proteins can be correlated with cell viability, state, health, etc.

Also embodied are methods to detect a protein complex of the present invention in cell culture models that express particular protein complexes or derivatives thereof, for the purpose of characterizing or preparing the complexes for harvest. This embodiment includes cell sorting of prokaryotes such as but not restricted to bacteria (Davey and Kell, 1996, *Microbiol. Rev.* 60:641-696), primary cultures and tissue specimens from eukaryotes, including mammalian species such as human (Steele et al., 1996, *Clin. Obstet. Gynecol.* 39:801-813), and continuous cell cultures (Orfao and Ruiz-Arguelles, 1996, *Clin. Biochem.* 29:5-9). Such isolations can be used as methods of diagnosis, described, *supra*.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

4.4 THERAPEUTIC USES OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The present invention is directed to a method for treatment or prevention of various diseases and disorders by administration of a therapeutic compound (termed herein "therapeutic"). Such "therapeutics" include, but are not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments) of the foregoing (e.g., as described hereinabove); antibodies thereto (as described hereinabove); nucleic acids encoding the component

protein, and analogs or derivatives, thereof (e.g., as described hereinabove); component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The protein complexes as identified herein can be implicated in processes which are implicated in or associated with pathological conditions.

Diseases and disorders which can be treated and/or prevented and/or diagnosed by therapeutics interacting with any of the complexes provided herein are for example neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders, inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease.

These disorders are treated or prevented by administration of a therapeutic that modulates (i.e. inhibits or promotes) protein complex activity or formation or modulates its function or composition. Diseases or disorders associated with aberrant levels of complex activity or formation, or aberrant levels or activity of the component proteins, or aberrant complex composition or a change in the function, may be treated by administration of a therapeutic that modulates complex formation or activity or by the administration of a protein complex.

Therapeutics may also be administered to modulate complex formation or activity or level thereof in a microbial organism such as yeast, fungi such as candida albicans causing an infectious disease in animals or humans.

Diseases and disorders characterized by increased (relative to a subject not suffering from the disease or disorder) complex levels or activity can be treated with therapeutics that antagonize (i.e., reduce or inhibit) complex formation or activity. Therapeutics that can be used include, but are not limited to, the component proteins or an analog, derivative or fragment of the component protein; anti-complex antibodies (e.g., antibodies specific for the protein complex, or a fragment or derivative of the antibody containing the binding region thereof; nucleic acids encoding the component proteins; antisense nucleic acids complementary to nucleic acids encoding the component proteins; and nucleic acids encoding the component protein that are dysfunctional due to, e.g., a heterologous insertion within the protein coding sequence, that are used to "knockout" endogenous protein function by homologous recombination, see, e.g., Capecchi, 1989, Science 244:1288-1292. In one embodiment, a therapeutic is 1, 2 or more antisense nucleic acids which are complementary to 1, 2, or more nucleic acids, respectfully, that encode component proteins of a complex.

In a specific embodiment of the present invention, a nucleic acid containing a portion of a component protein gene in which gene sequences flank (are both 5' and 3' to) a different gene sequence, is used as a component protein antagonist, or to promote component protein inactivation by homologous recombination (see also, Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342: 435-438). Additionally, mutants or derivatives of a component protein that has greater affinity for another component protein or the complex than wild type may be administered to compete with wild type protein for binding, thereby reducing the levels of complexes containing the wild type protein. Other therapeutics that inhibit complex function can be identified by use of known convenient *in vitro* assays, e.g., based on their ability to inhibit complex formation, or as described in Section 4.5, *infra*.

In specific embodiments, therapeutics that antagonize complex formation or activity are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an increased (relative to normal or desired) level of a complex, for example, in patients where complexes are overactive or overexpressed; or (2) in diseases or disorders where an *in vitro* (or *in vivo*) assay (see *infra*) indicates the utility of antagonist administration. Increased levels of a complex can be readily detected, e.g., by quantifying protein and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it *in vitro* for RNA or protein levels, or structure and/or activity of the expressed complex (or the encoding mRNA). Many methods standard in the art can be thus employed including, but not limited to, immunoassays to detect complexes and/or visualize complexes (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.), and/or hybridization assays to detect concurrent expression of component protein mRNA (e.g., Northern assays, dot blot analysis, *in situ* hybridization, etc.).

A more specific embodiment of the present invention is directed to a method of reducing complex expression (i.e., expression of the protein components of the complex and/or formation of the complex) by targeting mRNAs that express the protein moieties. RNA therapeutics currently fall within three classes, antisense species, ribozymes, or RNA aptamers (Good et al., 1997, *Gene Therapy* 4:45-54).

Antisense oligonucleotides have been the most widely used. By way of example, but not limitation, antisense oligonucleotide methodology to reduce complex formation is presented below, *infra*. Ribozyme therapy involves the administration, induced

expression, etc. of small RNA molecules with enzymatic ability to cleave, bind, or otherwise inactivate specific RNAs, to reduce or eliminate expression of particular proteins (Grassi and Marini, 1996, *Annals of Medicine* 28:499-510; Gibson, 1996, *Cancer and Metastasis Reviews* 15:287-299). RNA aptamers are specific RNA ligand proteins, such as for Tat and Rev RNA (Good et al., 1997, *Gene Therapy* 4:45-54) that can specifically inhibit their translation. Aptamers specific for component proteins can be identified by many methods well known in the art, for example, by affecting the formation of a complex in the protein-protein interaction assay described, *infra*.

In another embodiment, the activity or levels of a component protein are reduced by administration of another component protein, or the encoding nucleic acid, or an antibody that immunospecifically binds to the component protein, or a fragment or a derivative of the antibody containing the binding domain thereof.

In another aspect of the invention, diseases or disorders associated with increased levels of an component protein of the complex may be treated or prevented by administration of a therapeutic that increases complex formation if the complex formation acts to reduce or inactivate the component protein through complex formation. Such diseases or disorders can be treated or prevented by administration of one component member of the complex, administration of antibodies or other molecules that stabilize the complex, etc.

Diseases and disorders associated with underexpression of a complex, or a component protein, are treated or prevented by administration of a therapeutic that promotes (i.e., increases or supplies) complex levels and/or function, or individual component protein function. Examples of such a therapeutic include but are not limited to a complex or a derivative, analog or fragment of the complex that are functionally active (e.g., able to form a complex), un-complexed component proteins and derivatives, analogs, and fragments of un-complexed component proteins, and nucleic acids encoding the members of a complex or functionally active derivatives or fragments of the members of the complex, e.g., for use in gene therapy. In a specific embodiment, a therapeutic includes derivatives, homologs or fragments of a component protein that increase and/or stabilize complex formation. Examples of other agonists can be identified using *in vitro* assays or animal models, examples of which are described, *infra*.

In yet other specific embodiments of the present invention, therapeutics that promote complex function are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an absence or decreased (relative to normal or

desired) level of a complex, for example, in patients where a complex, or the individual components necessary to form the complex, is lacking, genetically defective, biologically inactive or underactive, or under-expressed; or (2) in diseases or disorders wherein an in vitro or in vivo assay (see, *infra*) indicates the utility of complex agonist administration. The absence or decreased level of a complex, component protein or function can be readily detected, e.g., by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it in vitro for RNA or protein levels, structure and/or activity of the expressed complex and/or the concurrent expression of mRNA encoding the two components of the complex. Many methods standard in the art can be thus employed, including but not limited to immunoassays to detect and/or visualize a complex, or the individual components of a complex (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs encoding the individual protein components of a complex by detecting and/or visualizing component mRNA concurrently or separately using, e.g., Northern assays, dot blot analysis, in situ hybridization, etc.

In specific embodiments, the activity or levels of a component protein are increased by administration of another component protein of the same complex, or a derivative, homolog or analog thereof, a nucleic acid encoding the other component, or an agent that stabilizes or enhances the other component, or a fragment or derivative of such an agent.

Generally, administration of products of species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, a human complex, or derivative, homolog or analog thereof; nucleic acids encoding the members of the human complex or a derivative, homolog or analog thereof; an antibody to a human complex, or a derivative thereof; or other human agents that affect component proteins or the complex, are therapeutically or prophylactically administered to a human patient.

Preferably, suitable in vitro or in vivo assays are utilized to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue or individual.

In various specific embodiments, in vitro assays can be carried out with representative cells of cell types involved in a patient's disorder, to determine if a therapeutic has a desired effect upon such cell types.

Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including, but not limited to, rats, mice, chicken, cows, monkeys, rabbits, etc. For in vivo testing, prior to administration to humans, any animal model system known in the art may be used. Additional descriptions and sources of therapeutics that can be used according to the invention are found in Sections 4.1 to 4.3 and 4.7 herein.

4.4.1 GENE THERAPY

In a specific embodiment of the present invention, nucleic acids comprising a sequence encoding the component proteins, or a functional derivative thereof, are administered to modulate complex activity or formation by way of gene therapy. Gene therapy refers to therapy performed by the administration of a nucleic acid to a subject. In this embodiment of the present invention, the nucleic acid expresses its encoded protein(s) that mediates a therapeutic effect by modulating complex activity or formation. Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, *Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217; and May, 1993, *TIBTECH* 11:155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al., eds., 1993, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; and Kriegler, 1990, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY.

In a preferred aspect, the therapeutic comprises a nucleic acid that is part of an expression vector that expresses one or more of the component proteins, or fragments or chimeric proteins thereof, in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the protein coding region(s) (or, less preferably separate promoters linked to the separate coding regions separately), said promoter being inducible or constitutive, and optionally, tissue-specific. In another particular embodiment, a nucleic acid molecule is used in which the coding sequences, and any other desired sequences, are flanked by regions that promote homologous

recombination at a desired site in the genome, thus providing for intra-chromosomal expression of the component protein nucleic acids (Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342:435-438).

Delivery of the nucleic acid into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vector, or indirect, in which case, cells are first transformed with the nucleic acid *in vitro*, then transplanted into the patient. These two approaches are known, respectively, as *in vivo* or *ex vivo* gene therapy.

In a specific embodiment, the nucleic acid is directly administered *in vivo*, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by infection using a defective or attenuated retroviral or other viral vector (U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors, or through use of transfecting agents, by encapsulation in liposomes, microparticles, or microcapsules, or by administering it in linkage to a peptide that is known to enter the nucleus, or by administering it in linkage to a ligand subject to receptor-mediated endocytosis that can be used to target cell types specifically expressing the receptors (e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432), etc. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide that disrupts endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (see, e.g., International Patent Publications WO 92/06180; WO 92/22635; WO 92/20316; WO 93/14188; and WO 93/20221. Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342:435-438).

In a specific embodiment, a viral vector that contains the component protein encoding nucleic acids is used. For example, a retroviral vector can be used (Miller et al., 1993, *Meth. Enzymol.* 217:581-599). These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The encoding nucleic acids to be used in gene therapy

is/are cloned into the vector, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., 1994, *Biotherapy* 6:291-302, which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are Clowes et al., 1994, *J. Clin. Invest.* 93:644-651; Kiem et al., 1994, *Blood* 83:1467-1473; Salmons and Gunzberg, 1993, *Human Gene Therapy* 4:129-141; and Grossman and Wilson, 1993, *Curr. Opin. in Genetics and Devel.* 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are the liver, the central nervous system, endothelial cells and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, *Curr. Opin. Genet. Devel.* 3:499-503, discuss adenovirus-based gene therapy. The use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys has been demonstrated by Bout et al., 1994, *Human Gene Therapy* 5:3-10. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, *Science* 252:431-434; Rosenfeld et al., 1992, *Cell* 68:143-155; and Mastrangeli et al., 1993, *J. Clin. Invest.* 91:225-234.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, *Proc. Soc. Exp. Biol. Med.* 204:289-300).

Another approach to gene therapy involves transferring a gene into cells in tissue culture by methods such as electroporation, lipofection, calcium phosphate-mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene from those that have not. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art including, but not limited to, transfection by electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the

introduction of foreign genes into cells (see, e.g., Loeffler and Behr, 1993, *Meth. Enzymol.* 217:599-618; Cohen et al., 1993, *Meth. Enzymol.* 217:618-644; Cline, 1985, *Pharmac. Ther.* 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably, is heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. In a preferred embodiment, epithelial cells are injected, e.g., subcutaneously. In another embodiment, recombinant skin cells may be applied as a skin graft onto the patient. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes, blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, and granulocytes, various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, a component protein encoding nucleic acid is/are introduced into the cells such that the gene or genes are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention. Such stem cells include but are not limited to hematopoietic stem cells (HSCs), stem cells of epithelial tissues such as the skin and the lining of the gut, embryonic heart muscle cells, liver stem cells (International Patent Publication WO 94/08598), and neural stem cells (Stemple and Anderson, 1992, *Cell* 71:973-985).

Epithelial stem cells (ESCs), or keratinocytes, can be obtained from tissues such as the skin and the lining of the gut by known procedures (Rheinwald, 1980, *Meth. Cell Biol.* 2A:229). In stratified epithelial tissue such as the skin, renewal occurs by mitosis of stem cells within the germinal layer, the layer closest to the basal lamina. Similarly, stem cells within the lining of the gut provide for a rapid renewal rate of this tissue. ESCs or keratinocytes obtained from the skin or lining of the gut of a patient or donor can be grown in tissue culture (Rheinwald, 1980, *Meth. Cell Bio.* 2A:229; Pittelkow and Scott, 1986, *Mayo Clinic Proc.* 61:771). If the ESCs are provided by a donor, a method for suppression of host versus graft reactivity (e.g., irradiation, or drug or antibody administration to promote moderate immunosuppression) can also be used.

With respect to hematopoietic stem cells (HSCs), any technique that provides for the isolation, propagation, and maintenance in vitro of HSCs can be used in this embodiment of the invention. Techniques by which this may be accomplished include (a) the isolation and establishment of HSC cultures from bone marrow cells isolated from the future host, or a donor, or (b) the use of previously established long-term HSC cultures, which may be allogeneic or xenogeneic. Non-autologous HSCs are used preferably in conjunction with a method of suppressing transplantation immune reactions between the future host and patient. In a particular embodiment of the present invention, human bone marrow cells can be obtained from the posterior iliac crest by needle aspiration (see, e.g., Kodo et al., 1984, *J. Clin. Invest.* 73: 1377-1384). In a preferred embodiment of the present invention, the HSCs can be made highly enriched or in substantially pure form. This enrichment can be accomplished before, during, or after long-term culturing, and can be done by any technique known in the art. Long-term cultures of bone marrow cells can be established and maintained by using, for example, modified Dexter cell culture techniques (Dexter et al., 1977, *J. Cell Physiol.* 91:335) or Witlock-Witte culture techniques (Witlock and Witte, 1982, *Proc. Natl. Acad. Sci. USA* 79:3608-3612).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

Additional methods can be adapted for use to deliver a nucleic acid encoding the component proteins, or functional derivatives thereof, e.g., as described in Section 4.1, *supra*.

4.4.2 USE OF ANTISENSE OLIGONUCLEOTIDES FOR SUPPRESSION OF PROTEIN COMPLEX FORMATION OR PROTEIN COMPLEX/PROTEIN ACTIVITY

In a specific embodiment of the present invention, protein complex activity and formation and protein activity is inhibited by use of antisense nucleic acids for the component proteins of the complex, that inhibit transcription and/or translation of their complementary sequence. The present invention provides the therapeutic or prophylactic use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding a component protein, or a portion thereof. An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific portion of a component protein RNA (preferably mRNA) by virtue of some sequence complementarity. The antisense nucleic acid may be complementary to a coding and/or noncoding region of a component protein mRNA. Such antisense nucleic acids that inhibit complex formation or activity have utility as therapeutics, and can be used in the treatment or prevention of disorders as described supra.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA, or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

In another embodiment, the present invention is directed to a method for inhibiting the expression of component protein nucleic acid sequences, in a prokaryotic or eukaryotic cell, comprising providing the cell with an effective amount of a composition comprising an antisense nucleic acid of the component protein, or a derivative thereof, of the invention.

The antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides, ranging from 6 to about 200 nucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures, or derivatives or modified versions thereof, and either single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents facilitating transport across the cell membrane (see,

e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Patent Publication No. WO 88/09810) or blood-brain barrier (see, e.g., International Patent Publication No. WO 89/10134), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position in its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thio-uridine, 5-carboxymethylaminomethyluracil, dihydrouracil, β -D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, β -D-mannosylqueosine, 5N-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methyl-thio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal, or an analog of the foregoing.

In yet another embodiment, the oligonucleotide is a 2'-*a*-anomeric oligonucleotide. An *a*-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligo-nucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451), etc.

In a specific embodiment, the antisense oligonucleotides comprise catalytic RNAs, or ribozymes (see, e.g., International Patent Publication No. WO 90/11364; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the antisense nucleic acids of the invention are produced intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced in vivo such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the component protein. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art to be capable of replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. USA 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a component protein gene, preferably a human gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a component protein RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The component protein antisense nucleic acids can be used to treat (or prevent) disorders of a cell type that expresses, or preferably overexpresses, a protein complex.

Cell types that express or overexpress component protein RNA can be identified by various methods known in the art. Such methods include, but are not limited to, hybridization with component protein-specific nucleic acids (e.g., by Northern blot hybridization, dot blot hybridization, or in situ hybridization), or by observing the ability of RNA from the cell type to be translated in vitro into the component protein by immunohistochemistry, Western blot analysis, ELISA, etc. In a preferred aspect, primary tissue from a patient can be assayed for protein expression prior to treatment, e.g., by immunocytochemistry, in situ hybridization, or any number of methods to detect protein or mRNA expression.

Pharmaceutical compositions of the invention (see Section 4.7, *infra*), comprising an effective amount of a protein component antisense nucleic acid in a pharmaceutically acceptable carrier can be administered to a patient having a disease or disorder that is of a type that expresses or overexpresses a protein complex of the present invention.

The amount of antisense nucleic acid that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the antisense cytotoxicity in vitro, and then in useful animal model systems, prior to testing and use in humans.

In a specific embodiment, pharmaceutical compositions comprising antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, it may be useful to use such compositions to achieve sustained release of the antisense nucleic acids. In a specific embodiment, it may be desirable to utilize liposomes targeted via antibodies to specific identifiable central nervous system cell types (Leonetti et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2448-2451; Renneisen et al., 1990, J. Biol. Chem. 265:16337-16342).

4.5 ASSAYS OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION AND DERIVATIVES AND ANALOGS THEREOF

The functional activity of a protein complex of the present invention, or a derivative, fragment or analog thereof or protein component thereof, can be assayed by various methods. Potential modulators (e.g., agonists and antagonists) of complex activity or formation, e.g., anti-complex antibodies and antisense nucleic acids, can be assayed for the ability to modulate complex activity or formation.

In one embodiment of the present invention, where one is assaying for the ability to bind or compete with a wild-type complex for binding to an anti-complex antibody, various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassay, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels), western blot analysis, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

The expression of the component protein genes (both endogenous and those expressed from cloned DNA containing the genes) can be detected using techniques

known in the art, including but not limited to Southern hybridization (Southern, 1975, J. Mol. Biol. 98:503-517), northern hybridization (see, e.g., Freeman et al., 1983, Proc. Natl. Acad. Sci. USA 80:4094-4098), restriction endonuclease mapping (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, New York), RNase protection assays (Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1997), DNA sequence analysis, and polymerase chain reaction amplification (PCR; U.S. Patent Nos. 4,683,202, 4,683,195, and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. USA 85:7652-7657; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220) followed by Southern hybridization with probes specific for the component protein genes, in various cell types. Methods of amplification other than PCR commonly known in the art can be employed. In one embodiment, Southern hybridization can be used to detect genetic linkage of component protein gene mutations to physiological or pathological states. Various cell types, at various stages of development, can be characterized for their expression of component proteins at the same time and in the same cells. The stringency of the hybridization conditions for northern or Southern blot analysis can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific probes used. Modifications to these methods and other methods commonly known in the art can be used.

Derivatives (e.g., fragments), homologs and analogs of one component protein can be assayed for binding to another component protein in the same complex by any method known in the art, for example the modified yeast matrix mating test described in Section 4.6.1 *infra*, immunoprecipitation with an antibody that binds to the component protein complexed with other component proteins in the same complex, followed by size fractionation of the immunoprecipitated proteins (e.g., by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western blot analysis, etc.

One embodiment of the invention provides a method for screening a derivative, homolog or analog of a component protein for biological activity comprising contacting said derivative, homolog or analog of the component protein with the other component proteins in the same complex; and detecting the formation of a complex between said derivative, homolog or analog of the component protein and the other component proteins; wherein detecting formation of said complex indicates that said derivative, homolog or analog of has biological (e.g., binding) activity.

The invention also provides methods of modulating the activity of a component protein that can participate in a protein complex by administration of a binding partner of that protein or derivative, homolog or analog thereof.

In a specific embodiment of the present invention, a protein complex of the present invention is administered to treat or prevent a disease or disorder, since the complex and/or component proteins have been implicated in the disease and disorder. Accordingly, a protein complex or a derivative, homolog, analog or fragment thereof, nucleic acids encoding the component proteins, anti-complex antibodies, and other modulators of protein complex activity, can be tested for activity in treating or preventing a disease or disorder in in vitro and in vivo assays.

In one embodiment, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by contacting cultured cells that exhibit an indicator of the disease in vitro, with the therapeutic, and comparing the level of said indicator in the cells contacted with the therapeutic, with said level of said indicator in cells not so contacted, wherein a lower level in said contacted cells indicates that the therapeutic has activity in treating or preventing the disease.

In another embodiment of the invention, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by administering the therapeutic to a test animal that is predisposed to develop symptoms of a disease, and measuring the change in said symptoms of the disease after administration of said therapeutic, wherein a reduction in the severity of the symptoms of the disease or prevention of the symptoms of the disease indicates that the therapeutic has activity in treating or preventing the disease. Such a test animal can be any one of a number of animal models known in the art for disease. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section 4.6 (supra) as exemplary animal models to study any of the complexes provided in the invention.

4.6 SCREENING FOR MODULATORS OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

A complex of the present invention, the component proteins of the complex and nucleic acids encoding the component proteins, as well as derivatives and fragments of the amino and nucleic acids, can be used to screen for compounds that bind to, or

modulate the amount of, activity of, or protein component composition of, said complex, and thus, have potential use as modulators, i.e., agonists or antagonists, of complex activity, and/or complex formation, i.e., the amount of complex formed, and/or protein component composition of the complex.

Thus, the present invention is also directed to methods for screening for molecules that bind to, or modulate the function of, amount of, activity of, formation of or protein component composition of, a complex of the present invention. In one embodiment of the invention, the method for screening for a molecule that modulates directly or indirectly the function, activity or formation of a complex of the present invention comprises exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules under conditions conducive to modulation; and determining the amount of, the biochemical activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on the function of the complex and/or product of a gene dependend on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on the function of the complex and/or product of a gene dependend on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

In another embodiment, the present invention further relates to a process for the identification and/or preparation of an effector of the complex comprising the step of bringing into contact a product of any of claims 1 to 8 with a compound, a mixture or a library of compounds and determining whether the compound or a certain compound of the mixture or library binds to the product and/or effects the products biological activity and optionally further purifying the compound positively tested as effector.

In another embodiment, the present invention is directed to a method for screening for a molecule that binds a protein complex of the present invention comprising exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules; and determining whether said complex is bound by any of said candidate molecules. Such screening assays can be carried out using cell-free and cell-based methods that are commonly known in the art in vitro, in vivo or ex vivo. For example, an isolated complex can be employed, or a cell can be contacted with the candidate molecule and the complex can be isolated from such contacted cells and the isolated complex can be assayed for activity or component composition. In another example, a cell containing the complex can be contacted with

the candidate molecule and the levels of the complex in the contacted cell can be measured. Additionally, such assays can be carried out in cells recombinantly expressing a component protein from the third column of table 1, or a functionally active fragment or functionally active derivative thereof, and a component protein from fourth column of table 1, or a functionally active fragment or functionally active derivative thereof. Additionally, such assays can also be carried out in cells recombinantly expressing all component proteins from the group of proteins in the fifth column of table 1.

For example, assays can be carried out using recombinant cells expressing the protein components of a complex, to screen for molecules that bind to, or interfere with, or promote complex activity or formation. In preferred embodiments, polypeptide derivatives that have superior stabilities but retain the ability to form a complex (e.g., one or more component proteins modified to be resistant to proteolytic degradation in the binding assay buffers, or to be resistant to oxidative degradation), are used to screen for modulators of complex activity or formation. Such resistant molecules can be generated, e.g., by substitution of amino acids at proteolytic cleavage sites, the use of chemically derivatized amino acids at proteolytic susceptible sites, and the replacement of amino acid residues subject to oxidation, i.e. methionine and cysteine.

A particular aspect of the present invention relates to identifying molecules that inhibit or promote formation or degradation of a complex of the present invention, e.g., using the method described for isolating the complex and identifying members of the complex using the TAP assay described in Section 4, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety.

In another embodiment of the invention, a modulator is identified by administering a candidate molecule to a transgenic non-human animal expressing the complex component proteins from promoters that are not the native promoters of the respective proteins, more preferably where the candidate molecule is also recombinantly expressed in the transgenic non-human animal. Alternatively, the method for identifying such a modulator can be carried out *in vitro*, preferably with a purified complex, and a purified candidate molecule.

Agents/molecules (candidate molecules) to be screened can be provided as mixtures of a limited number of specified compounds, or as compound libraries, peptide libraries and the like. Agents/molecules to be screened may also include all forms of

antisera, antisense nucleic acids, etc., that can modulate complex activity or formation. Exemplary candidate molecules and libraries for screening are set forth in Section 4.6.1, *infra*.

Screening the libraries can be accomplished by any of a variety of commonly known methods. See, e.g., the following references, which disclose screening of peptide libraries: Parmley and Smith, 1989, *Adv. Exp. Med. Biol.* 251:215-218; Scott and Smith, 1990, *Science* 249:386-390; Fowlkes et al., 1992, *BioTechniques* 13:422-427; Oldenburg et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:5393-5397; Yu et al., 1994, *Cell* 76:933-945; Staudt et al., 1988, *Science* 241:577-580; Bock et al., 1992, *Nature* 355:564-566; Tuerk et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:6988-6992; Ellington et al., 1992, *Nature* 355:850-852; U.S. Patent No. 5,096,815, U.S. Patent No. 5,223,409, and U.S. Patent No. 5,198,346, all to Ladner et al.; Rebar and Pabo, 1993, *Science* 263:671-673; and International Patent Publication No. WO 94/18318.

In a specific embodiment, screening can be carried out by contacting the library members with a complex immobilized on a solid phase, and harvesting those library members that bind to the protein (or encoding nucleic acid or derivative). Examples of such screening methods, termed "panning" techniques, are described by way of example in Parmley and Smith, 1988, *Gene* 73:305-318; Fowlkes et al., 1992, *BioTechniques* 13:422-427; International Patent Publication No. WO 94/18318; and in references cited hereinabove.

In a specific embodiment, fragments and/or analogs of protein components of a complex, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex formation (amount of complex or composition of complex) or activity in the cell, which thereby inhibit complex activity or formation in the cell.

In one embodiment, agents that modulate (i.e., antagonize or agonize) complex activity or formation can be screened for using a binding inhibition assay, wherein agents are screened for their ability to modulate formation of a complex under aqueous, or physiological, binding conditions in which complex formation occurs in the absence of the agent to be tested. Agents that interfere with the formation of complexes of the invention are identified as antagonists of complex formation. Agents that promote the formation of complexes are identified as agonists of complex formation. Agents that completely block the formation of complexes are identified as inhibitors of complex formation.

Methods for screening may involve labeling the component proteins of the complex with radioligands (e.g., ^{125}I or ^3H), magnetic ligands (e.g., paramagnetic beads covalently attached to photobiotin acetate), fluorescent ligands (e.g., fluorescein or rhodamine), or enzyme ligands (e.g., luciferase or β -galactosidase). The reactants that bind in solution can then be isolated by one of many techniques known in the art, including but not restricted to, co-immunoprecipitation of the labeled complex moiety using antisera against the unlabeled binding partner (or labeled binding partner with a distinguishable marker from that used on the second labeled complex moiety), immunoaffinity chromatography, size exclusion chromatography, and gradient density centrifugation. In a preferred embodiment, the labeled binding partner is a small fragment or peptidomimetic that is not retained by a commercially available filter. Upon binding, the labeled species is then unable to pass through the filter, providing for a simple assay of complex formation.

Methods commonly known in the art are used to label at least one of the component members of the complex. Suitable labeling methods include, but are not limited to, radiolabeling by incorporation of radiolabeled amino acids, e.g., ^3H -leucine or ^{35}S -methionine, radiolabeling by post-translational iodination with ^{125}I or ^{131}I using the chloramine T method, Bolton-Hunter reagents, etc., or labeling with ^{32}P using phosphorylase and inorganic radiolabeled phosphorous, biotin labeling with photobiotin-acetate and sunlamp exposure, etc. In cases where one of the members of the complex is immobilized, e.g., as described infra, the free species is labeled. Where neither of the interacting species is immobilized, each can be labeled with a distinguishable marker such that isolation of both moieties can be followed to provide for more accurate quantification, and to distinguish the formation of homomeric from heteromeric complexes. Methods that utilize accessory proteins that bind to one of the modified interactants to improve the sensitivity of detection, increase the stability of the complex, etc., are provided.

Typical binding conditions are, for example, but not by way of limitation, in an aqueous salt solution of 10-250 mM NaCl, 5-50 mM Tris-HCl, pH 5-8, and 0.5% Triton X-100 or other detergent that improves specificity of interaction. Metal chelators and/or divalent cations may be added to improve binding and/or reduce proteolysis. Reaction temperatures may include 4, 10, 15, 22, 25, 35, or 42 degrees Celsius, and time of incubation is typically at least 15 seconds, but longer times are preferred to allow binding

equilibrium to occur. Particular complexes can be assayed using routine protein binding assays to determine optimal binding conditions for reproducible binding.

The physical parameters of complex formation can be analyzed by quantification of complex formation using assay methods specific for the label used, e.g., liquid scintillation counting for radioactivity detection, enzyme activity for enzyme-labeled moieties, etc. The reaction results are then analyzed utilizing Scatchard analysis, Hill analysis, and other methods commonly known in the arts (see, e.g., *Proteins, Structures, and Molecular Principles*, 2nd Edition (1993) Creighton, Ed., W.H. Freeman and Company, New York).

In a second common approach to binding assays, one of the binding species is immobilized on a filter, in a microtiter plate well, in a test tube, to a chromatography matrix, etc., either covalently or non-covalently. Proteins can be covalently immobilized using any method well known in the art, for example, but not limited to the method of Kadonaga and Tjian, 1986, *Proc. Natl. Acad. Sci. USA* 83:5889-5893, i.e., linkage to a cyanogen-bromide derivatized substrate such as CNBr-Sepharose 4B (Pharmacia). Where needed, the use of spacers can reduce steric hindrance by the substrate. Non-covalent attachment of proteins to a substrate include, but are not limited to, attachment of a protein to a charged surface, binding with specific antibodies, binding to a third unrelated interacting protein, etc.

Assays of agents (including cell extracts or a library pool) for competition for binding of one member of a complex (or derivatives thereof) with another member of the complex labeled by any means (e.g., those means described above) are provided to screen for competitors or enhancers of complex formation.

In specific embodiments, blocking agents to inhibit non-specific binding of reagents to other protein components, or absorptive losses of reagents to plastics, immobilization matrices, etc., are included in the assay mixture. Blocking agents include, but are not restricted to bovine serum albumin, β -casein, nonfat dried milk, Denhardt's reagent, Ficoll, polyvinylpyrrolidone, nonionic detergents (NP40, Triton X-100, Tween 20, Tween 80, etc.), ionic detergents (e.g., SDS, LDS, etc.), polyethylene glycol, etc. Appropriate blocking agent concentrations allow complex formation.

After binding is performed, unbound, labeled protein is removed in the supernatant, and the immobilized protein retaining any bound, labeled protein is washed extensively. The amount of bound label is then quantified using standard methods in the art to detect the label as described, *supra*.

In another specific embodiments screening for modulators of the protein complexes/protein as provided herein can be carried out by attaching those and/or the antibodies as provided herein to a solid carrier. In a further specific embodiment, the invention relates to an array of said molecules.

The preparation of such an array containing different types of proteins, including antibodies) is well known in the art and is apparent to a person skilled in the art (see e.g. Ekins et al., 1989, *J. Pharm. Biomed. Anal.* 7:155-168; Mitchell et al. 2002, *Nature Biotechnol.* 20:225-229; Petricoin et al., 2002, *Lancet* 359:572-577; Templin et al., 2001, *Trends Biotechnol.* 20:160-166; Wilson and Nock, 2001, *Curr. Opin. Chem. Biol.* 6:81-85; Lee et al., 2002 *Science* 295:1702-1705; MacBeath and Schreiber, 2000, *Science* 289:1760; Blawas and Reichert, 1998, *Biomaterials* 19:595; Kane et al., 1999, *Biomaterials* 20:2363; Chen et al., 1997, *Science* 276:1425; Vaughan et al., 1996, *Nature Biotechnol.* 14:309-314; Mahler et al., 1997, *Immunotechnology* 3:31-43; Roberts et al., 1999, *Curr. Opin. Chem. Biol.* 3:268-273; Nord et al., 1997, *Nature Biotechnol.* 15:772-777; Nord et al., 2001, *Eur. J. Biochem.* 268:4269-4277; Brody and Gold, 2000, *Rev. Mol. Biotechnol.* 74:5-13; Karlstroem and Nygren, 2001, *Anal. Biochem.* 295:22-30; Nelson et al., 2000, *Electrophoresis* 21:1155-1163; Honore et al., 2001, *Expert Rev. Mol. Diagn.* 3:265-274; Albala, 2001, *Expert Rev. Mol. Diagn.* 2:145-152, Figeys and Pinto, 2001, *Electrophoresis* 2:208-216 and references in the publications listed here).

Complexes can be attached to an array by different means as will be apparent to a person skilled in the art. Complexes can for example be added to the array via a TAP-tag (as described in WO/0009716 and in Rigaut et al., 1999, *Nature Biotechnol.* 10:1030-1032) after the purification step or by another suitable purification scheme as will be apparent to a person skilled in the art.

Optionally, the proteins of the complex can be cross-linked to enhance the stability of the complex. Different methods to cross-link proteins are well known in the art. Reactive end-groups of cross-linking agents include but are not limited to -COOH, -SH, -NH₂ or N-oxy-succinamate.

The spacer of the cross-linking agent should be chosen with respect to the size of the complex to be cross-linked. For small protein complexes, comprising only a few proteins, relatively short spacers are preferable in order to reduce the likelihood of cross-linking separate complexes in the reaction mixture. For larger protein complexes, additional use of larger spacers is preferable in order to facilitate cross-linking between proteins within the complex.

It is preferable to check the success-rate of cross-linking before linking the complex to the carrier.

As will be apparent to a person skilled in the art, the optimal rate of cross-linking need to be determined on a case by case basis. This can be achieved by methods well known in the art, some of which are exemplary described below.

A sufficient rate of cross-linking can be checked f.e. by analysing the cross-linked complex vs. a non-cross-linked complex on a denaturing protein gel.

If cross-linking has been performed successfully, the proteins of the complex are expected to be found in the same lane, whereas the proteins of the non-cross-linked complex are expected to be separated according to their individual characteristics. Optionally the presence of all proteins of the complex can be further checked by peptide-sequencing of proteins in the respective bands using methods well known in the art such as mass spectrometry and/or Edman degradation.

In addition, a rate of crosslinking which is too high should also be avoided. If cross-linking has been carried out too extensively, there will be an increasing amount of cross-linking of the individual protein complex, which potentially interferes with a screening for potential binding partners and/or modulators etc. using the arrays. The presence of such structures can be determined by methods well known in the art and include e.g. gel-filtration experiments comparing the gel filtration profile solutions containing cross-linked complexes vs. uncross-linked complexes.

Optionally, functional assays as will be apparent to a person skilled in the art, some of which are exemplarily provided herein, can be performed to check the integrity of the complex.

Alternatively, members of the protein complex can be expressed as a single fusion protein and coupled to the matrix as will be apparent to a person skilled in the art.

Optionally, the attachment of the complex or proteins or antibody as outlined above can be further monitored by various methods apparent to a person skilled in the art. Those include, but are not limited to surface plasmon resonance (see e.g. McDonnel, 2001, Curr. Opin. Chem. Biol. 5:572-577; Lee, 2001, Trends Biotechnol. 19:217-222; Weinberger et al., 2000, 1:395-416; Pearson et al., 2000, Ann. Clin. Biochem. 37:119-145; Vely et al., 2000, Methods Mol. Biol. 121:313-321; Slepak, 2000, J. Mol. Recognit. 13:20-26.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex, include but are not limited to those described in Vassar R et al., 1999, Science, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex include but are not limited to those described in Yan R et al., 1999, Nature, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex include but are not limited to those described in Tian G et al., 2002, J Biol Chem, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, PTK7-complex, BACE1-complex, include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

4.6.1 CANDIDATE MOLECULES

Any molecule known in the art can be tested for its ability to modulate (increase or decrease) the amount of, activity of, or protein component composition of a complex of the present invention as detected by a change in the amount of, activity of, or protein component composition of, said complex. By way of example, a change in the amount of the complex can be detected by detecting a change in the amount of the complex that can be isolated from a cell expressing the complex machinery. For identifying a

molecule that modulates complex activity, candidate molecules can be directly provided to a cell expressing the complex machinery, or, in the case of candidate proteins, can be provided by providing their encoding nucleic acids under conditions in which the nucleic acids are recombinantly expressed to produce the candidate proteins within the cell expressing the complex machinery, the complex is then isolated from the cell and the isolated complex is assayed for activity using methods well known in the art, not limited to those described, *supra*.

This embodiment of the invention is well suited to screen chemical libraries for molecules which modulate, e.g., inhibit, antagonize, or agonize, the amount of, activity of, or protein component composition of the complex. The chemical libraries can be peptide libraries, peptidomimetic libraries, chemically synthesized libraries, recombinant, e.g., phage display libraries, and in vitro translation-based libraries, other non-peptide synthetic organic libraries, etc.

Exemplary libraries are commercially available from several sources (ArQule, Tripos/PanLabs, ChemDesign, Pharmacopoeia). In some cases, these chemical libraries are generated using combinatorial strategies that encode the identity of each member of the library on a substrate to which the member compound is attached, thus allowing direct and immediate identification of a molecule that is an effective modulator. Thus, in many combinatorial approaches, the position on a plate of a compound specifies that compound's composition. Also, in one example, a single plate position may have from 1-20 chemicals that can be screened by administration to a well containing the interactions of interest. Thus, if modulation is detected, smaller and smaller pools of interacting pairs can be assayed for the modulation activity. By such methods, many candidate molecules can be screened.

Many diversity libraries suitable for use are known in the art and can be used to provide compounds to be tested according to the present invention. Alternatively, libraries can be constructed using standard methods. Chemical (synthetic) libraries, recombinant expression libraries, or polysome-based libraries are exemplary types of libraries that can be used.

The libraries can be constrained or semirigid (having some degree of structural rigidity), or linear or unconstrained. The library can be a cDNA or genomic expression library, random peptide expression library or a chemically synthesized random peptide library, or non-peptide library. Expression libraries are introduced into the cells in which

the assay occurs, where the nucleic acids of the library are expressed to produce their encoded proteins.

In one embodiment, peptide libraries that can be used in the present invention may be libraries that are chemically synthesized in vitro. Examples of such libraries are given in Houghten et al., 1991, *Nature* 354:84-86, which describes mixtures of free hexapeptides in which the first and second residues in each peptide were individually and specifically defined; Lam et al., 1991, *Nature* 354:82-84, which describes a "one bead, one peptide" approach in which a solid phase split synthesis scheme produced a library of peptides in which each bead in the collection had immobilized thereon a single, random sequence of amino acid residues; Medynski, 1994, *Bio/Technology* 12:709-710, which describes split synthesis and T-bag synthesis methods; and Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251. Simply by way of other examples, a combinatorial library may be prepared for use, according to the methods of Ohlmeyer et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:10922-10926; Erb et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:11422-11426; Houghten et al., 1992, *Biotechniques* 13:412; Jayawickreme et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:1614-1618; or Salmon et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:11708-11712. PCT Publication No. WO 93/20242 and Brenner and Lerner, 1992, *Proc. Natl. Acad. Sci. USA* 89:5381-5383 describe "encoded combinatorial chemical libraries," that contain oligonucleotide identifiers for each chemical polymer library member.

In a preferred embodiment, the library screened is a biological expression library that is a random peptide phage display library, where the random peptides are constrained (e.g., by virtue of having disulfide bonding).

Further, more general, structurally constrained, organic diversity (e.g., nonpeptide) libraries, can also be used. By way of example, a benzodiazepine library (see e.g., Bunin et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:4708-4712) may be used.

Conformationally constrained libraries that can be used include but are not limited to those containing invariant cysteine residues which, in an oxidizing environment, cross-link by disulfide bonds to form cystines, modified peptides (e.g., incorporating fluorine, metals, isotopic labels, are phosphorylated, etc.), peptides containing one or more non-naturally occurring amino acids, non-peptide structures, and peptides containing a significant fraction of γ -carboxyglutamic acid.

Libraries of non-peptides, e.g., peptide derivatives (for example, that contain one or more non-naturally occurring amino acids) can also be used. One example of these

are peptoid libraries (Simon et al., 1992, Proc. Natl. Acad. Sci. USA 89:9367-9371). Peptoids are polymers of non-natural amino acids that have naturally occurring side chains attached not to the α carbon but to the backbone amino nitrogen. Since peptoids are not easily degraded by human digestive enzymes, they are advantageously more easily adaptable to drug use. Another example of a library that can be used, in which the amide functionalities in peptides have been permethylated to generate a chemically transformed combinatorial library, is described by Ostresh et al., 1994, Proc. Natl. Acad. Sci. USA 91:11138-11142).

The members of the peptide libraries that can be screened according to the invention are not limited to containing the 20 naturally occurring amino acids. In particular, chemically synthesized libraries and polysome based libraries allow the use of amino acids in addition to the 20 naturally occurring amino acids (by their inclusion in the precursor pool of amino acids used in library production). In specific embodiments, the library members contain one or more non-natural or non-classical amino acids or cyclic peptides. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, β -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid; β -Abu, β -Ahx, 6-amino hexanoic acid; Aib, 2-amino isobutyric acid; 3-amino propionic acid; ornithine; norleucine; norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, designer amino acids such as β -methyl amino acids, γ -methyl amino acids, N-methyl amino acids, fluoro-amino acids and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, fragments and/or analogs of complexes of the invention, or protein components thereof, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex activity or formation.

In another embodiment of the present invention, combinatorial chemistry can be used to identify modulators of the complexes. Combinatorial chemistry is capable of creating libraries containing hundreds of thousands of compounds, many of which may be structurally similar. While high throughput screening programs are capable of screening these vast libraries for affinity for known targets, new approaches have been developed that achieve libraries of smaller dimension but which provide maximum chemical diversity. (See e.g., Matter, 1997, J. Med. Chem. 40:1219-1229).

One method of combinatorial chemistry, affinity fingerprinting, has previously been used to test a discrete library of small molecules for binding affinities for a defined

panel of proteins. The fingerprints obtained by the screen are used to predict the affinity of the individual library members for other proteins or receptors of interest (in the instant invention, the protein complexes of the present invention and protein components thereof.) The fingerprints are compared with fingerprints obtained from other compounds known to react with the protein of interest to predict whether the library compound might similarly react. For example, rather than testing every ligand in a large library for interaction with a complex or protein component, only those ligands having a fingerprint similar to other compounds known to have that activity could be tested. (See, e.g., Kauvar et al., 1995, Chem. Biol. 2:107-118; Kauvar, 1995, Affinity fingerprinting, Pharmaceutical Manufacturing International. 8:25-28; and Kauvar, Toxic-Chemical Detection by Pattern Recognition in New Frontiers in Agrochemical Immunoassay, Kurtz, Stanker and Skerritt (eds), 1995, AOAC: Washington, D.C., 305-312).

Kay et al. (1993, Gene 128:59-65) disclosed a method of constructing peptide libraries that encode peptides of totally random sequence that are longer than those of any prior conventional libraries. The libraries disclosed in Kay et al. encode totally synthetic random peptides of greater than about 20 amino acids in length. Such libraries can be advantageously screened to identify complex modulators. (See also U.S. Patent No. 5,498,538 dated March 12, 1996; and PCT Publication No. WO 94/18318 dated August 18, 1994).

A comprehensive review of various types of peptide libraries can be found in Gallop et al., 1994, J. Med. Chem. 37:1233-1251.

4.7 PHARMACEUTICAL COMPOSITIONS AND THERAPEUTIC/PROPHYLACTIC ADMINISTRATION

The invention provides methods of treatment (and prophylaxis) by administration to a subject of an effective amount of a therapeutic of the invention. In a preferred aspect, the therapeutic is substantially purified. The subject is preferably an animal including, but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

Various delivery systems are known and can be used to administer a therapeutic of the invention, e.g., encapsulation in liposomes, microparticles, and microcapsules: use

of recombinant cells capable of expressing the therapeutic, use of receptor-mediated endocytosis (e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432); construction of a therapeutic nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion, by bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral, rectal and intestinal mucosa, etc.), and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment. This may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

In another embodiment, the therapeutic can be delivered in a vesicle, in particular a liposome (Langer, 1990, *Science* 249:1527-1533; Treat et al., 1989, In: *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler, eds., Liss, New York, pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the therapeutic can be delivered via a controlled release system. In one embodiment, a pump may be used (Langer, *supra*; Sefton, 1987, *CRC Crit. Ref. Biomed. Eng.* 14:201-240; Buchwald et al., 1980, *Surgery* 88:507-516; Saudek et al., 1989, *N. Engl. J. Med.* 321:574-579). In another embodiment, polymeric materials can be used (*Medical Applications of Controlled Release*, Langer and Wise, eds., CRC Press, Boca Raton, Florida, 1974; *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball, eds., Wiley, New York, 1984;

Ranger and Peppas, 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61; Levy et al., 1985, *Science* 228:190-192; During et al., 1989, *Ann. Neurol.* 25:351-356; Howard et al., 1989, *J. Neurosurg.* 71:858-863). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (e.g., Goodson, 1984, In: *Medical Applications of Controlled Release*, supra, Vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer (1990, *Science* 249:1527-1533).

In a specific embodiment where the therapeutic is a nucleic acid encoding a protein therapeutic, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or by coating it with lipids, cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (e.g., Joliet et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:1864-1868), etc. Alternatively, a nucleic acid therapeutic can be introduced intracellularly and incorporated by homologous recombination within host cell DNA for expression.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a therapeutic, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride,

dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated, in accordance with routine procedures, as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water or saline for injection can be provided so that the ingredients may be mixed prior to administration.

The therapeutics of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free carboxyl groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., those formed with free amine groups such as those derived from isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc., and those derived from sodium, potassium, ammonium, calcium, and ferric hydroxides, etc.

The amount of the therapeutic of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or

condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. For example, the kit can comprise in one or more containers a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group consisting of proteins listed in the third column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fourth column of table 1.

Alternatively, the kit can comprise in one or more containers, all proteins, functionally active fragments or functionally active derivatives thereof of from the group of proteins in the fifth column of table 1.

The kits of the present invention can also contain expression vectors encoding the essential components of the complex machinery, which components after being expressed can be reconstituted in order to form a biologically active complex. Such a kit preferably also contains the required buffers and reagents. Optionally associated with such container(s) can be instructions for use of the kit and/or a notice in the form

prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

4.8 ANIMAL MODELS

The present invention also provides animal models. In one embodiment, animal models for diseases and disorders involving the protein complexes of the present invention are provided. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section 4.6 (supra) as exemplary animal models to study any of the complexes provided in the invention. Such animals can be initially produced by promoting homologous recombination or insertional mutagenesis between genes encoding the protein components of the complexes in the chromosome, and exogenous genes encoding the protein components of the complexes that have been rendered biologically inactive or deleted (preferably by insertion of a heterologous sequence, e.g., an antibiotic resistance gene). In a preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which a gene encoding a component protein from the third column of table 1, or a functionally active fragment or functionally active derivative thereof, and a gene encoding a component protein from the fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, has been inactivated or deleted (Capecchi, 1989, Science 244:1288-1292).

In another preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which the genes of all component proteins from the group of proteins listed in the third column of table 1 or of all proteins from the group of proteins listed in the forth column of table 1 have been inactivated or deleted.

The chimeric animal can be bred to produce additional knockout animals. Such animals can be mice, hamsters, sheep, pigs, cattle, etc., and are preferably non-human mammals. In a specific embodiment, a knockout mouse is produced.

Such knockout animals are expected to develop, or be predisposed to developing, diseases or disorders associated with mutations involving the protein complexes of the present invention, and thus, can have use as animal models of such diseases and disorders, e.g., to screen for or test molecules (e.g., potential therapeutics) for such diseases and disorders.

In a different embodiment of the invention, transgenic animals that have incorporated and express (or over-express or mis-express) a functional gene encoding a protein component of the complex, e.g. by introducing the a gene encoding one or more of the components of the complex under the control of a heterologous promoter (i.e., a promoter that is not the native promoter of the gene) that either over-expresses the protein or proteins, or expresses them in tissues not normally expressing the complexes or proteins, can have use as animal models of diseases and disorders characterized by elevated levels of the protein complexes. Such animals can be used to screen or test molecules for the ability to treat or prevent the diseases and disorders cited supra.

In one embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group of proteins listed in the third column of table 1, and an endogenous gene encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fourth column of table 1 has been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof. In addition, the present invention provides a recombinant non-human animal in which the endogenous genes of all proteins, or functionally active fragments or functionally active derivatives thereof of one of the group of proteins listed in the fifth column have been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof:

In another embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group consisting of proteins of the third column of table 1, and endogenous gene

encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins of the fourth column, of table 1 are recombinantly expressed in said animal or an ancestor thereof.

The following series of examples are presented by way of illustration and not by way of limitation on the scope of the invention.

EXAMPLES

An object of the present invention was to identify protein complexes of the APP processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the complexes of the APP processing pathway and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

By applying the process according to the invention said complexes were identified. The components are listed in table 1.

Thus, the invention relates to the following embodiments:

Thus the invention relates to the

The invention further relates to the Nicastrin complex (a):

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a

nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(v) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and

(vi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a

nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,

(v) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(vi) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(vii) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(viii) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(ix) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(x) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xi) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xiv) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xv) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xvi) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xvii) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xviii) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xix) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a

nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xx) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxi) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

(xxii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxiii) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxiv) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxv) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxvi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxvii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxviii) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and

(xxx) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C , washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55°C , and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C .

2. The protein complex according to No. 1 wherein the first protein is the protein "Nicastrin" (SEQ ID No:9), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid under low stringency conditions.

3. The protein complex according to No. 1 comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical

protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, (xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING

finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 29 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a

nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,

(vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181"

encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1"

encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several

interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:

expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Nicastrin complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Nicastrin complex selected from

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,
- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and
- (xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C , washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55°C , and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C .

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising:

- (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
- (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or

functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,
- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, comprising the steps of:

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:

- (a) exposing said complex, or a cell or organism containing Nicastrin complex to one or more candidate molecules; and
- (b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of

said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions, and/or

- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions, and/or

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions, and/or

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions, and/or

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions, and/or

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

- (xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, and/or
- (xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or
- (xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or
- (xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a

nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes

to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

- (vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342"

encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions, and/or

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions, and/or

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions, and/or

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions, and/or

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, and/or

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,

(vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical

protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, (xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING

finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxlii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the Nicastrin-complex (b):

1. A protein complex selected from complex (I) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a

nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(ii) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(v) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and

(vi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (v) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (vi) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (vii) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (viii) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (ix) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (x) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xii) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xiii) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xiv) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xviii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xix) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxiv) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxv) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxvi) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxvii) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, (xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes

to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and

(xxxvii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'Nicastrin' (SEQ ID NO. 147), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Nicastrin' encoded by a nucleic acid that hybridizes to the 'Nicastrin' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

- (xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2"

encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes

to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (vi) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (viii) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (x) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (xi) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiii) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xix) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

- (xxi) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xxv) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,
- (xxvi) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxvii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xxviii) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxix) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxx) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxv) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xl) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 36 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that

hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

- "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

- (xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

- (xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,
- (xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,
- (xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
- (xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions,

(xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the

interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Nicastrin complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Nicastrin complex selected from

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the

"ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a

functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342"

encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a

functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a

functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390"

encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a

functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a

functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922"

encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof,

or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181

(FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181

(FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof,

or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533

(FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533

(FRAGMENT)" nucleic acid or its complement under low stringency conditions,

- (xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,
- (xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and
- (xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said

proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Nicastrin complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or

- (xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain

dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or

- (xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain

dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that

modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
 (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic

acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

- (xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a

nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin"

encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or(xliii) "tyrosine phosphatase

ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the present invention relates to the Nicastrin-complex (c)

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,

(xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and

(b) at least one first protein selected from the group consisting of:

(i) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

- (iii) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,
- (iv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,
- (v) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vi) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (vii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (ix) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (x) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xi) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363"

encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xiv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xv) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xviii) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xix) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

- (xx) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,
- (xxi) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,
- (xxii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,
- (xxiii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,
- (xxiv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,
- (xxv) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,
- (xxvi) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,
- (xxvii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA,

0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein APP-C99 (SEQ ID No:120), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'APP-C99' encoded by a nucleic acid that hybridizes to the 'APP-C99' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

- (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,
- (iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a

nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2"

encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-27 of the following proteins:

- (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,
- (iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a

nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,

(xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,

(xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

- (xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,
- (xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,
- (xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2"

encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the

expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.

13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or

functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.

16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.

17. The kit according to No. 16 for processing a substrate of said complex.

18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a

nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,

- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,
- (xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,
- (xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

- (xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,
- (xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,
- (xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,
- (xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,
- (xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,
- (xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,
- (xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,
- (xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1"

encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing Nicastrin-complex to one or more candidate molecules; and
(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions, and/or

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions, and/or

- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a

nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or (xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament

for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions, and/or

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions, and/or

- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a

nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21"

encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several

interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

- (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,
- (iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a

nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

- (xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,
- (xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,
- (xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,
- (xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,
- (xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,
- (xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,
- (xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2"

encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

The invention further relates to the following embodiments of the Bace1-complex (a)

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and
 - (ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and
 - (b) at least one second protein, which second protein is selected from the group consisting of:
 - (i) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
 - (ii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
 - (iii) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,
 - (iv) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,
 - (v) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

- (vi) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (viii) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (x) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,
- (xi) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xii) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (xiii) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,
- (xiv) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO

Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,

(xv) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,

(xvi) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,

(xvii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xviii) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and

(xix) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Bace1 (SEQ ID NO. 129), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Bace1' encoded by a nucleic acid that hybridizes to the 'Bace1' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,

(v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668"

encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,

(xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,

- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,
- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,
- (xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,
- (xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,
- (xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 18 of the following proteins:

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,
- (v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,
- (vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

- (x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,
- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,
- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,
- (xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-

related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,

(xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the

interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the BACE1 complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the BACE1 complex selected from

- (i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668"

encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and

(vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being

selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, comprising the steps of

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing BACE1 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether
 (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions, and/or

(v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or

(vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or

(vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions, and/or

(viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249"

encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions, and/or

(ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions, and/or

(x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or

(xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or

(xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions, and/or

(xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions, and/or

- (ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions, and/or
- (x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a

nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions, and/or

(xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means

of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1"

encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,

(v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,

- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,
- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,
- (xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,
- (xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,
- (xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or (xxi) "kinectin 1 (kinesin receptor)" (SEQ ID

No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the present invention relates to the BACE1-complex (b)

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and

(b) at least one first protein selected from the group consisting of:

(i) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(ii) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,
- (v) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (vi) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (vii) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (viii) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (ix) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (x) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xi) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a

nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xii) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xiii) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,

(xiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xv) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xvi) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xvii) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xviii) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xix) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xx) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxi) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxiv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein BACE1 (SEQ ID No:38), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'BACE1' encoded by a nucleic acid that hybridizes to the 'BACE1' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,
- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,
- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin"

encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xxi) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-24 of the following proteins:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid

that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,
- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,
- (xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,
- (xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,
- (xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,
- (xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha"

encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in

cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members. ●

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11. ●

13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).
15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.
16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.
17. The kit according to No. 16 for processing a substrate of said complex.
18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.
19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.
20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.
21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:
- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,
- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a

nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xvi) "LAPTM4B" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B" encoded by a nucleic acid that hybridizes to the "LAPTM4B" nucleic acid or its complement under low stringency conditions,

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

- (xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,
- (xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,
- (xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,
- (xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,
- (xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,
- (xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,
- (xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,
- (xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1"

encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions., and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of: (a) exposing said complex, or a cell or organism containing BACE1-complex to one or more candidate molecules; and (b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or

(v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or

(vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or

(vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin"

encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions, and/or

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions, and/or

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions, and/or

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not

having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or

- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49"

encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions, and/or

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions, and/or

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions, and/or

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions, and/or

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying

the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a

nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,
- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,
- (xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,
- (xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a

nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

Furthermore, the present invention relates to the Psen2-complex

1. A protein complex selected from complex (not defined) and comprising
 - (a) at least one first protein selected from the group consisting of:

- (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,
- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and
- (b) at least one first protein selected from the group consisting of:
 - (i) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
 - (ii) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
 - (iii) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
 - (iv) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
 - (v) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

- (vi) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (viii) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (x) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xi) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,
- (xii) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,
- (xiii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,
- (xiv) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2"

encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xv) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xvi) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xvii) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xviii) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xix) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xx) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxi) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxiii) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxiv) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxv) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Psen2 (SEQ ID No:121), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Psen2' encoded by a nucleic acid that hybridizes to the 'Psen2' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a

nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

- (xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,
- (xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,
- (xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,
- (xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,
- (xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,
- (xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a

nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-25 of the following proteins:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a

nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a

nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in

cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.

13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.

16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.

17. The kit according to No. 16 for processing a substrate of said complex.

18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,
- (x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin"

encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,
 (xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing Psen2-complex to one or more candidate molecules; and
 (b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said

complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions, and/or

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a

nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions, and/or

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions, and/or

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a

nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions, and/or

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a

nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions, and/or

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

- (xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a

nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

- (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,
- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579"

encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xviii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

- (xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,
- (xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,
- (xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,
- (xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,
- (xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,
- (xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,
- (xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,
- (xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,
- (xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD"

encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

Furthermore, the present invention relates to the PTK7-complex

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and

(b) at least one first protein selected from the group consisting of:

(i) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(ii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a

nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(iii) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(iv) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(v) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,

(vi) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(vii) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(viii) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein PTK7 (SEQ ID No:44), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'PTK7' encoded by a nucleic acid that hybridizes to the 'PTK7' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

- (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,

(viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-8 of the following proteins:

(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,
- (x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.
13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a

functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.

16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.

17. The kit according to No. 16 for processing a substrate of said complex.

18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing PTK7-complex to one or more candidate molecules; and
(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated

complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

(v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(vii) "HIFPH3/EGLN3" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions, and/or

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular

localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether
(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid

that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

(v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions, and/or

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,
- (x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

5. PROTOCOLS:

The TAP-technology, which is more fully described in EP 1 105 508 B1 and in Rigaut, et al., 1999, Nature Biotechnol. 17:1030-1032 respectively was used and further adapted as described below for protein purification. Proteins were identified using mass spectrometry as described further below.

5.1 Construction of TAP-tagged bait

The cDNAs encoding the complete ORF were obtained by RT-PCR. Total RNA was prepared from appropriate cell lines using the RNeasy Mini Kit (Qiagen). Both cDNA synthesis and PCR were performed with the SUPERSCRIPT One-Step RT-PCR for Long templates Kit (Life Technologies) using gene-specific primers. After 35-40 cycles of amplification PCR-products with the expected size were gel-purified with the MinElute PCR Purification Kit (Qiagen) and, if necessary, used for further amplification. Low-abundant RNAs were amplified by nested PCR before gel-purification. Restriction sites for NotI were attached to PCR primers to allow subcloning of amplified cDNAs into the retroviral vectors pIE94-N/C-TAP thereby generating N- or C-terminal fusions with the TAP-tag (Rigaut et al., 1999, Nature Biotechnol. 17:1030-1032). N-terminal tagging was chosen for the following baits/entry points: Presenilin 1, Presenilin 2, Aph-1a, Aph-1b, Pen-2, APP, Tau, Fe65, Calsenilin. C-terminal tagging was chosen for the following baits/entry points: Nicastrin, Aph-1a, Aph-1b, BACE1 D215N, APP, APP695SW, APP-C99, Fe65, X11beta.

Clones were analyzed by restriction digest, DNA sequencing and by in vitro translation using the TNT T7 Quick Coupled Transcription/Translation System (Promega inc.). The presence of the proteins was proven by Western blotting using the protein A part of the TAP-tag for detection. Briefly, separation of proteins by standard SDS-PAGE was followed by semi-dry transfer onto a nitrocellulose membrane (PROTRAN, Schleicher&Schuell) using the MultiphorII blotting apparatus from Pharmacia Biotech. The transfer buffer consisted of 48 mM Tris, 39 mM glycine, 10% methanol and 0,0375% sodium dodecylsulfate. After blocking in phosphate-buffered saline (PBS) supplemented

with 10% dry milk powder and 0,1% Tween 20 transferred proteins were probed with the Peroxidase-Anti-Peroxidase Soluble Complex (Sigma) diluted in blocking solution. After intensive washing immunoreactive proteins were visualized by enhanced chemiluminescence (ECL; Amersham Pharmacia Biotech).

5.2 Preparation of Virus and infection

As a vector, a MoMLV-based recombinant virus was used.

The preparation has been carried out as follows:

5.2.1 Preparation of Virus

293 gp cells were grown to 100% confluency. They were split 1:5 on poly-L-Lysine plates (1:5 diluted poly-L-Lysine [0.01% stock solution, Sigma P-4832] in PBS, left on plates for at least 10 min.). On Day 2, 63 microgram of retroviral Vector DNA together with 13 microgram of DNA of plasmid encoding an appropriate envelope protein were transfected into 293 gp cells (Somia, et al., 1999, Proc. Natl. Acad. Sci. USA 96:12667-12672; Somia, et al. 2000, J. Virol. 74:4420-4424). On Day 3, the medium was replaced with 15 ml DMEM + 10% FBS per 15-cm dish. On Day 4, the medium containing viruses (supernatant) was harvested (at 24 h following medium change after transfection). When a second collection was planned, DMEM 10 % FBS was added to the plates and the plates were incubated for another 24 h. All collections were done as follows: The supernatant was filtered through 0.45 micrometer filter (Corning GmbH, cellulose acetate, 431155). The filter was placed into konical polyallomer centrifuge tubes (Beckman, 358126) that are placed in buckets of a SW 28 rotor (Beckman). The filtered supernatant was ultracentrifuged at 19400 rpm in the SW 28 rotor, for 2 hours at 21 degree Celsius. The supernatant was discarded. The pellet containing viruses was resuspended in a small volume (for example 300 microliter) of Hank's Balanced Salt Solution [Gibco BRL, 14025-092], by pipetting up and down 100-times, using an aerosol-safe tip. The viruses were used for transfection as described below.

5.2.2 Infection

Cells that were infected were plated one day before into one well of a 6-well plate. 4 hours before infection, the old medium on the cells was replaced with fresh medium. Only a minimal volume was added, so that the cells are completely covered (e.g. 700 microliter). During infection, the cells were actively dividing.

A description of the cells and their growth conditions is given in 5.2.3

To the concentrated virus, polybrene (Hexadimethrine Bromide; Sigma, H 9268) was added to achieve a final concentration of 8 microgram/ml (this is equivalent to 2.4 microliter of the 1 milligram/ml polybrene stock per 300 microliter of concentrated retrovirus). The virus was incubated in polybrene at room temperature for 1 hour. For infection, the virus/polybrene mixture was added to the cells and incubated at 37 degree Celsius at the appropriate CO₂ concentration for several hours (e.g. over-day or over-night). Following infection, the medium on the infected cells was replaced with fresh medium. The cells were passaged as usual after they became confluent. The cells contain the retrovirus integrated into their chromosomes and stably express the gene of interest.

5.2.3 Cell lines

For expression, SKN-BE2 cells were used. SKN-BE2 cells (American Type Culture Collection-No. CRL-2271) were grown in 95% OptiMEM + 5% iron-supplemented calf serum.

The expression pattern of the TAP-tagged proteins was checked by immunoblot-analysis as described in 5.3.3 and/or by immunofluorescence as described in 5.3.1 or 5.3.2.

5.3 Checking of expression pattern of TAP-tagged proteins

The expression pattern of the TAP-tagged protein was checked by immunoblot analysis and/or by immunofluorescence. Immunofluorescence analysis was either carried out according to section 5.3.1 or to section 5.3.2 depending on the type of the TAP-tagged protein. Immunoblot analysis was carried out according to section 5.3.3.

5.3.1 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for plasma membrane and ER bound proteins

Cells were grown in FCS media on polylysine coated 8 well chamber slides to 50% confluency. Then fixation of the cells was performed in 4% ParaFormAldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4). The cells were incubated for 30 minutes at room temperature in 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Blocking was performed with 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at room temperature. Incubation of the primary antibodies was performed in the blocking solution overnight at +4°C. The proper dilution of the antibodies was determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin for 2x 20 minutes at room temperature. Incubation of the secondary antibodies is performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes). Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin was used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were then washed again 2x 20 minutes at room temperature in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

5.3.2 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for non-plasma membrane bound proteins:

Cells were grown in FCS media on Polylysine coated 8 well chamber slides to 50% confluency. Fixation of the cells was performed in 4% ParaFormAldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4) for 30

minutes at Room Temperature (RT), 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Permeabilization of cells was done with 0.5% Triton X-100 in PBS for 10 minutes at room temperature. Blocking was then done in 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at RT (Blocking solution). Incubation of the primary antibodies was performed in the blocking solution, overnight at +4°C. The proper dilution of the antibodies has to be determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin, for 2x 20 minutes at RT. Incubation of the secondary antibodies was performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes), Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin is used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were washed 2x 20 minutes at RT in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

5.3.3 Immunoblot analysis

To analyze expression levels of TAP-tagged proteins, a cell pellet (from a 6-well dish) was lysed in 60 μ l DNase I buffer (5% Glycerol, 100 mM NaCl, 0.8 % NP-40 (IGEPAL), 5 mM magnesium sulfate, 100 μ g/ml DNase I (Roche Diagnostics), 50 mM Tris, pH 7.5, protease inhibitor cocktail) for 15 min on ice. Each sample was split into two aliquots. The first half was centrifuged at 13,000 rpm for 5 min. to yield the NP-40-extractable material in the supernatant; the second half (total material) was carefully triturated. 50 μ g each of the NP-40-extractable material and the total material are mixed with DTT-containing sample buffer for 30 min at 50°C on a shaker and separated by SDS polyacrylamide gel electrophoresis on a precast 4-12% Bis-Tris gel (Invitrogen). Proteins were then transferred to nitrocellulose using a semi-dry procedure with a discontinuous buffer system. Briefly, gel and nitrocellulose membrane were stacked between filter papers soaked in either anode buffer (three layers buffer A1 (0.3 M Tris-HCl) and three layers buffer A2 (0.03 M Tris-HCl)) or cathode buffer (three layers of 0.03 M Tris-HCl, pH 9.4, 0.1 % SDS, 40 mM ϵ -aminocaproic acid). Electrotransfer of two gels at once was performed at 600 mA for 25 min. Transferred proteins were visualized with Ponceau S solution for one min to control transfer efficiency and then destained in water. The

membrane was blocked in 5% non-fat milk powder in TBST (TBS containing 0.05% Tween-20) for 30 min at room temperature. It was subsequently incubated with HRP-coupled PAP antibody (1:5000 diluted in 5% milk/TBST) for 1 h at room temperature, washed three times for 10 min in TBST. The blot membrane was finally soaked in chemiluminescent substrate (ECL, Roche Diagnostics) for 2 min. and either exposed to X-ray film or analyzed on an imaging station.

5.4 Purification of protein complexes

Protein complex purification was adapted to the sub-cellular localization of the TAP-tagged protein and was performed as described below.

5.4.1 Lysate preparation for cytoplasmic proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of CZ lysis buffer (50 mM Tris-Cl, pH 7.4; 5 % Glycerol; 0,2 % IGEPAL; 1.5 mM $MgCl_2$; 100 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was incubated for 30 min on ice and spun for 10 min at 20,000g. The supernatant was subjected to an additional ultracentrifugation step for 1 h at 100,000g. The supernatant was recovered and rapidly frozen in liquid nitrogen or immediately processed further.

5.4.2 Lysate preparation for membrane proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Membrane-Lysis buffer (50 mM Tris, pH 7.4; 7.5 % Glycerol; 1 mM EDTA;

150 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 750g, the supernatant was recovered and subjected to an ultracentrifugation step for 1 h at 100,000g. The membrane pellet was resuspended in 7,5 ml of Membrane-Lysis buffer containing 0.8% n-Dodecyl- β -D-maltoside and incubated for 1 h at 4°C with constant agitation. The sample was subjected to another ultracentrifugation step for 1h at 100,000g and the solubilized material was quickly frozen in liquid nitrogen or immediately processed further.

5.4.3 Lysate preparation for nuclear proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Hypotonic-Lysis buffer (10 mM Tris, pH 7.4; 1.5 mM MgCl_2 ; 10 mM KCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 2,000g and the resulting supernatant (S1) saved on ice. The nuclear pellet (P1) was resuspended in 5 ml Nuclear-Lysis buffer (50 mM Tris, pH 7.4; 1.5 mM MgCl_2 ; 20 % Glycerol; 420 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and incubated for 30 min on ice. The sample was combined with S1, further diluted with 7 ml of Dilution buffer (110 mM Tris, pH 7.4; 0.7 % NP40; 1.5 mM MgCl_2 ; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT), incubated on ice for 10 min and centrifuged at 100,000g for 1h. The final supernatant (S2) was frozen quickly in liquid nitrogen.

5.4.4 Tandem Affinity Purification

The frozen lysate was quickly thawed in a 37°C water bath, and spun for 20 min at 100,000g. The supernatant was recovered and incubated with 0.2 ml of settled rabbit

IgG-Agarose beads (Sigma) for 2 h with constant agitation at 4°C. Immobilized protein complexes were washed with 10 ml of CZ lysis buffer (containing 1 Complete™ tablet (Roche) per 50 ml of buffer) and further washed with 5 ml of TEV cleavage buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 0.5 mM EDTA; 1 mM DTT). Protein-complexes were eluted by incubation with 5 µl of TEV protease (GibcoBRL, Cat.No. 10127-017) for 1 h at 16°C in 150 µl TEV cleavage buffer. The eluate was recovered and combined with 0.2 ml settled Calmodulin affinity beads (Stratagene) in 0.2 ml CBP binding buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 2mM MgAc; 2mM Imidazole; 1mM DTT; 4 mM CaCl₂) followed by 1 h incubation at 4°C with constant agitation. Immobilized protein complexes were washed with 10 ml of CBP wash buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 1mM MgAc; 1mM Imidazole; 1mM DTT; 2 mM CaCl₂) and eluted by addition of 600 µl CBP elution buffer (10 mM Tris, pH 8.0; 5 mM EGTA) for 5 min at 37°C. The eluate was recovered in a siliconized tube and lyophilized. The remaining Calmodulin resin was boiled for 5 min in 50 µl 4x Laemmli sample buffer. The sample buffer was isolated, combined with the lyophilised fraction and loaded on a NuPAGE gradient gel (Invitrogen, 4-12%, 1.5 mm, 10 well).

5.5 Protein Identification by Mass Spectrometry

5.5.1 Protein digestion prior to mass spectrometric analysis

Gel-separated proteins were reduced, alkylated and digested in gel essentially following the procedure described by Shevchenko et al., 1996, Anal. Chem. 68:850-858. Briefly, gel-separated proteins were excised from the gel using a clean scalpel, reduced using 10 mM DTT (in 5mM ammonium bicarbonate, 54°C, 45 min) and subsequently alkylated with 55 mM iodoacetamid (in 5 mM ammonium bicarbonate) at room temperature in the dark (30 min). Reduced and alkylated proteins were digested in gel with porcine trypsin (Promega) at a protease concentration of 12.5 ng/µl in 5mM ammonium bicarbonate. Digestion was allowed to proceed for 4 hours at 37°C and the reaction was subsequently stopped using 5 µl 5% formic acid.

5.5.2 Sample preparation prior to analysis by mass spectrometry

Gel plugs were extracted twice with 20 μ l 1% TFA and pooled with acidified digest supernatants. Samples were dried in a vacuum centrifuge and resuspended in 13 μ l 1% TFA.

5.5.3 Mass spectrometric data acquisition

Peptide samples were injected into a nano LC system (CapLC, Waters or Ultimate, Dionex) which was directly coupled either to a quadrupole TOF (QTOF2, QTOF Ultima, QTOF Micro, Micromass or QSTAR Pulsar, Sciex) or ion trap (LCQ Deca XP) mass spectrometer. Peptides were separated on the LC system using a gradient of aqueous and organic solvents (see below). Solvent A was 5% acetonitrile in 0.5% formic acid and solvent B was 70% acetonitrile in 0.5% formic acid.

Time (min)	% solvent A	% solvent B
0	95	5
5.33	92	8
35	50	50
36	20	80
40	20	80
41	95	5
50	95	5

Peptides eluting off the LC system were partially sequenced within the mass spectrometer.

5.5.4 Protein identification

The peptide mass and fragmentation data generated in the LC-MS/MS experiments were used to query fasta formatted protein and nucleotide sequence databases maintained and updated regularly at the NCBI (for the NCBI nr, dbEST and the human and mouse genomes) and European Bioinformatics Institute (EBI, for the human, mouse, *D. melanogaster* and *C. elegans* proteome databases). Proteins were identified by correlating the measured peptide mass and fragmentation data with the same data

computed from the entries in the database using the software tool Mascot (Matrix Science; Perkins et al., 1999, Electrophoresis 20:3551-3567). Search criteria varied depending on which mass spectrometer was used for the analysis.

5.6. siRNA-Inhibition of FADS2, DEGS, SCD4

FADS2, DEGS and SCD4 were separately inhibited by siRNA-expression. Results are depicted in figures 3, 5, 7.

siRNAs for human FADS2 were synthesized by Dharmacon Research Inc.

The sequences used for FADS2 are:

GCUGAAAUACCUGCCCUAC and GCAUGGCAUUGAAUACCAG

Transfection of SK-N-BE2 cells was performed using LipofectAMINE 2000 (Invitrogen) following the manufacturer's instructions. Briefly, the cells were seeded at a density of 1.0×10^4 cells in a final volume of 85 μ l per 96-well 12-16 hrs prior to transfection. 25 nM of siRNAs were mixed with 8 μ l Opti-MEM buffer (Gibco) and 60 ng carrier DNA, and the mixture was incubated for 20 minutes at room temperature before addition to the cells. 16 and 48 hrs post-transfection medium was replaced with 100 μ l or 200 μ l growth medium with or without serum, respectively. 72 hrs post-transfection 100 μ l supernatants were harvested for A β 42 ELISA. The assay was performed following the manufacturer's instructions (Innogenetics).

Transfection of H4 cells was performed using RNAiFect (Qiagen) following the manufacturer's instructions. Briefly, the cells were seeded at a density of 1.0×10^4 cells in a final volume of 100 μ l per 96-well 12-16 hrs prior to transfection. 270 nM (0,375 μ g) of siRNAs were mixed with 25 μ l EC-R buffer and 2,3 μ l of RNAiFect and incubated for 15 minutes at room temperature before addition to the cells. During complex formation medium on cells was replaced with 75 μ l of fresh growth medium. 5 hrs post-transfection the cells were washed once with growth medium and 100 μ l were added for further cultivation. 48 hrs post-transfection medium was replaced with 200 μ l serum-free growth medium. 72 hrs post-transfection 100 μ l supernatants were harvested for A β 42 ELISA. The assay was performed following the manufacturer's instructions (Innogenetics).

Knockdown efficiency of selected siRNAs was assessed at the protein level by co-transfecting siRNAs and corresponding TAP-tagged cDNA expression vectors or by using cell lines stably expressing the respective tagged protein of interest. 48 hrs post-transfection extracts were prepared, proteins separated by SDS-PAGE and transferred to nitrocellulose. Western blots were probed with antibodies directed against the tag and tubulin.

5.7. Determination of FADS2-activity

a) . Rat liver microsomal assay

(Obukowicz MG, Raz A, Pyla PD, Rico JG, Wendling JM, Needleman P (1998a)

Identification and characterization of a novel delta6/delta5 fatty acid desaturase inhibitor as a potential anti-inflammatory agent. *Biochem. Pharmacol.* 1;55(7): 1045-58;

Obukowicz MG, Welsch DJ, Salsgiver WJ, Martin-Berger CL, Chinn KS, Duffin KL, Raz A, Needleman P (1998b) Novel, selective delta6 or delta5 fatty acid desaturase inhibitors as antiinflammatory agents in mice. *J. Pharmacol. Exp. Ther.* 287(1):157-66)

Rat microsomal membranes are obtained by standard biochemical fractionation procedures.

In a 48-well plate the following components are mixed: a) 150 μ l buffer/cofactors (250 mM sucrose, 150 mM KCl, 40 mM NaF, 1.3 mM ATP, 1 mg/ml MgCl₂ * 5 H₂O, 1.5 mM reduced glutathione, 60 μ M reduced CoA, 330 μ M nicotinamide, 670 μ g/ml NADH, 100 mM sodium phosphate, pH 7.4); b) 50 μ l rat liver micro-somes (~500 μ g total protein); c) 2.2 μ l test compound (DMSO stock; 1% final DMSO concentration); d) 20 μ l (0.05 μ Ci) ¹⁴C-Fatty Acid Substrates.

Preferred substrate for FADS2 is α -linolenic acid (¹⁴C18:3n-3). [The assay allows for simultaneous measurement of FADS1 (Δ 5 desaturase) and SCD-1 activity (Δ 9 desaturase). The substrates for these enzymatic activities are ¹⁴C20:3n-3 and stearic acid (¹⁴C18:0), respectively.]

Samples are incubated at 37°C for 1 hr, and then reactions are stopped and fatty acid ester linkages hydrolyzed by incubation with 200 μ l 2.5N KOH in methanol:water (4:1) for 4 h at 65°C. Free fatty acids are protonated with 280 μ l formic acid and extracted into organic phase (700 μ l hexane). 200 μ l from hexane layer are analyzed on AgNO₃-thin-

layer chromatography (TLC) plates. Plates are dried over night and activity is quantified by phosphorimager. As an alternative to TLC analysis, separation of samples could be achieved by HPLC.

b) Cellular assay

A cell line expressing high levels of FADS2 (such as ABMC-7 mastocytoma cells) is utilized. Cells are adapted to grow in serum-free HL-1 medium containing FADS2 substrates (such as 10 μ M linoleic acid/15 μ M fatty acid-free BSA). To measure FADS2 activity 2 x 10⁵ cells are plated per 48-well and then incubated in medium containing 10 μ M of a suitable substrate (such as α -linolenic acid (¹⁴C18:3n-3)). To terminate fatty acid metabolism, the cell layer is washed with PBS and 200 μ l 2.5N KOH in methanol:water (4:1) are added. Samples are further processed as described above.

c) High-throughput screening assays using fatty acid synthetic enzymes (s. WO-03/019146, p.27 ff.)

The assay utilizes position-specifically tritiated fatty acyl-CoA esters in a microsome assay format (see above). The method detects the release of tritiated water and circumvents the requirement of TLC- or HPLC analysis of ¹⁴C-labeled fatty acids. For screening of FADS2 inhibitors suitable substrates (1 mCi/ml stock) are ³H [6,9,12-octadecadienoic acid] (CoA conjugate of linoleic acid) and/or ³H [9,12,15-octadecatrienoic acid] (CoA α -linolenic acid). The label should be position-specific at C6/C7.

Briefly, the following components are mixed (total volume: 100 μ l): 2 μ l unlabeled 1.5 mM fatty acyl CoA, 1 μ l tritiated fatty acyl CoA, 10 μ l 20 mM NADH, compounds from DMSO stock, 67 μ l 100 mM phosphate buffer, pH 7.2. 80 μ l of this mix are added to 20 μ l of microsomes (~20 μ g total protein) and reaction is allowed to proceed for 5-30 min at RT. 10 μ l 6% perchloric acid are added to stop the reaction. To sediment unused tritiated substrate, samples are vortexed with 100 μ l charcoal suspension and centrifuged at 13,000rpm for 10min at 4°C. 400 μ l of supernatant is analyzed in a liquid scintillation counter.

TABLE 1

COMPONENTS OF COMPLEXES

Name of complex	Entry Point	All interactors of the complex	Known interactors of the complex	Novel interactors of the complex	Proteins of unknown function
Nicastrin complex (a)	Nicastrin	18 kDa microsomal signal peptidase subunit	Aph-1a	18 kDa microsomal signal peptidase subunit	ATP-binding cassette, sub-family A, member 3
		25 kDa microsomal signal peptidase subunit	BACE1	25 kDa microsomal signal peptidase subunit	CGI-13
		Aph-1a	Nicastrin	ATP-binding cassette, sub-family A, member 3	ENSG00000144840
		ATP-binding cassette, sub-family A member 3	Pen-2	BSCv protein	FLJ20342
		BACE1	Presenilin-1	Casein kinase II beta chain	FLJ20481
		BSCv protein	Presenilin-2	Cathepsin B	FLJ22390
		Casein kinase II beta chain		CGI-13	Hypothetical protein tyrosine

					phosphatase ensg000000149185
		Cathepsin B			KIAA1181
		CGI-13			KIAA1533
		Delta-6 fatty acid desaturase			PP1, regulatory subunit 15B
		ENSG000000144840			RING finger protein 5
		FLJ13977			Thioredoxin domain-containing protein
		FLJ20342			
		FLJ20481			
		FLJ22390			
		Hypothetical protein tyrosine phosphatase ensg000000149185			
		ICAM-2			
		KIAA1181			
		Hypothetical protein tyrosine phosphatase ensg000000149185			
		ICAM-2			
		KIAA1181			
		Mesenchymal stem			

				cell protein DSCD75	
		KIAA1533		Neurotrypsin	
		Mesenchymal stem cell protein DSCD75		NICE-3	
		Neurotrypsin		Protein amplified in osteosarcoma (OS-9)	
		Nicastrin		PP1, regulatory subunit 15B	
		NICE-3		Protein similar to stromal cell-derived factor 2	
		Pen-2		Protocadherin beta 8	
		Presenilin-1		REP8 protein	
		Presenilin-2		Retinal short-chain dehydrogenase/reductase retSDR2	
		Protein amplified in osteosarcoma (OS-9)		RING finger protein 5	
		PP1, regulatory subunit 15B		Stromal cell-derived factor 2-like 1	
		Protein similar to stromal cell-derived		Thioredoxin domain-containing protein	

		factor 2				
		Protocadherin beta 8			Voltage-dependent anion channel 1	
		REP8 protein				
		Retinal short-chain dehydrogenase/reductase retSDR2				
		RING finger protein 5				
		Stromal cell-derived factor 2-like 1				
		Thioredoxin domain-containing protein				
		Voltage-dependent anion channel 1				
Nicastrin-complex (b)	Nicastrin	18 kDa microsomal signal peptidase subunit			18 kDa microsomal signal peptidase subunit	
		25 kDa microsomal signal peptidase subunit			25 kDa microsomal signal peptidase subunit	
		Aph-1a		Aph-1a		
		ATP-binding cassette,			ATP-binding cassette,	ATP-binding

	sub-family A, member 3		sub-family A, member 3	cassette, sub-family A, member 3
	BACE1	BACE1		
	BSCv protein (FRAGMENT)		BSCv protein (FRAGMENT)	
	CAMK4		CAMK4	
	Casein kinase II beta chain		Casein kinase II beta chain	
	Cathepsin B		Cathepsin B	
	CGI-13		CGI-13	CGI-13
	DCTN1		DCTN1	
	Delta-6 fatty acid desaturase		Delta-6 fatty acid desaturase	
	ENSG000000144840		ENSG000000144840	ENSG000000144840
	FACL3		FACL3	0
	FACL4		FACL4	
	FLJ13977		FLJ13977	
	FLJ20342		FLJ20342	FLJ20342
	FLJ20481		FLJ20481	FLJ20481
	FLJ22390		FLJ22390	FLJ22390
	homolog of yeast golgi		homolog of yeast golgi	

	membrane protein yif1p (yip1p-interacting factor)		membrane protein yip1p (yip1p-interacting factor)	
	ICAM-2		ICAM-2	
	KIAA0095		KIAA0095	KIAA0095
	KIAA0922		KIAA0922	KIAA0922
	KIAA1181 (FRAGMENT)		KIAA1181 (FRAGMENT)	KIAA1181 (FRAGMENT)
	KIAA1533 (FRAGMENT)		KIAA1533 (FRAGMENT)	KIAA1533 (FRAGMENT)
	Mesenchymal stem cell protein DSCD75		Mesenchymal stem cell protein DSCD75	
	Neurotrypsin		Neurotrypsin	
	Nicastrin	Nicastrin		
	NICE-3		NICE-3	
	PAS domain containing serine/threonine kinase		PAS domain containing serine/threonine kinase	
	Pen-2	Pen-2		
	PP1, regulatory subunit 15B		PP1, regulatory subunit 15B	PP1, regulatory subunit 15B

	Presenilin-1	Presenilin-1		
	Presenilin-2	Presenilin-2		
	Protein amplified in osteosarcoma (OS-9)		Protein amplified in osteosarcoma (OS-9)	
	Protein similar to stromal cell-derived factor 2		Protein similar to stromal cell-derived factor 2	
	Protocadherin beta 8		Protocadherin beta 8	
	REP8 protein		REP8 protein	
	Retinal short-chain dehydrogenase/reductase retSDR2		Retinal short-chain dehydrogenase/reductase retSDR2	
	RING finger protein 5		RING finger protein 5	RING finger protein 5
	Stromal cell-derived factor 2-like 1		Stromal cell-derived factor 2-like 1	
	Thioredoxin domain-containing protein		Thioredoxin domain-containing protein	Thioredoxin domain-containing protein
	tyrosine phosphatase ensg00000149185		tyrosine phosphatase ensg00000149185	tyrosine phosphatase ensg00000149185

Nicastrin-complex (c)	Nicastrin	Nicastrin	Nicastrin
	Psen1		Psen1
	aph-1a		aph-1a
	APP		APP
	CtnnA1		CtnnA1
	CtnnA2		CtnnA2
	CtnnB1		CtnnB1
	CtnnD1		CtnnD1
	JUP		JUP
	NCadh		NCadh
	ACAT1		ACAT1
	CGI-13		CGI-13
	CK2B		CK2B
	CLGN		CLGN
	ECSIT		ECSIT
	FACL3		FACL3
	FADS2		FADS2
	FLJ20481		FLJ20481
	ITM2C		ITM2C
	ITPR1		ITPR1
	KIAA0363		KIAA0363

	MDR1		MDR1	
	Neurotrypsin		Neurotrypsin	
	PTP LOC114971		PTP LOC114971	
	RetSDR2		RetSDR2	
	SFXN1		SFXN1	
	SPC18		SPC18	
	SPC22		SPC22	
	SPC25		SPC25	
	SPTLC2		SPTLC2	
	stearoyl-CoA desaturase		stearoyl-CoA desaturase	
	STT3		STT3	
	TMP21		TMP21	
	UGCGL1		UGCGL1	
	visinin-like 1		visinin-like 1	
	Wolframin		Wolframin	
	YME1L1		YME1L1	
BACE1 (new)-complex (a)	BACE1	BACE1		
	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2

		Calsyntenin 1		Calsyntenin 1	
		CGI-13		CGI-13	
		Delta-6 fatty acid desaturase		Delta-6 fatty acid desaturase	
		Delta-like homolog		Delta-like homolog	
		FLJ30668		FLJ30668	FLJ30668
		FLJ39249		FLJ39249	FLJ39249
		integral membrane transporter protein		integral membrane transporter protein	
		ITCH		ITCH	
		KIAA1250		KIAA1250	KIAA1250
		kinectin 1 (kinesin receptor)		kinectin 1 (kinesin receptor)	
		Nicastrin	Nicastrin		
		Nogo-A		Nogo-A	
		PDGFRB		PDGFRB	
		PTK7		PTK7	
		SERPINA1		SERPINA1	
		SIM TO Y71H10A. 2.P.		SIM TO Y71H10A. 2.P.	SIM TO Y71H10A. 2.P.
		Sortilin-related receptor		Sortilin-related receptor	
		STX10		STX10	
		Thioredoxin domain-containing protein		Thioredoxin domain-containing protein	Thioredoxin

						domain-containing protein
BACE1-complex (b)	BACE1	APP	APP			
		Nicastrin			Nicastrin	
		ACAT1			ACAT1	
		APLP2			APLP2	
		BRI			BRI	
		calsyntenin 1			calsyntenin 1	
		CELSR2			CELSR2	
		CGI-13			CGI-13	
		DLK1			DLK1	
		DSCD75			DSCD75	
		FADS2			FADS2	
		GPR49			GPR49	
		ITM2C			ITM2C	
		KiDins220			KiDins220	
		LAPTM4B			LAPTM4B	
		Neurotrypsin			Neurotrypsin	
		NogoA			NogoA	
		OS-9			OS-9	
		PDGFRB			PDGFRB	

		PTK7			PTK7	
		RetSDR2			RetSDR2	
		S100alpha			S100alpha	
		SORL1			SORL1	
		stearoyl-CoA desaturase			stearoyl-CoA desaturase	
		TMP21				
		UGCL1				
Psen2- complex	Psen2	aph-1a		aph-1a		
		Nicastrin			Nicastrin	
		Nicastrin			Nicastrin	
		CGI-13			CGI-13	
		DSCD75			DSCD75	
		ECSIT			ECSIT	
		FACL3			FACL3	
		FADS2			FADS2	
		FLJ10579			FLJ10579	
		FLJ20481			FLJ20481	
		ITPR1			ITPR1	
		KIAA0090			KIAA0090	
		MDR1			MDR1	
		NicAChRa3			NicAChRa3	

		PLD3		PLD3	
		SFXN1		SFXN1	
		SLC4A2		SLC4A2	
		SORT1		SORT1	
		SPC18		SPC18	
		SPC22		SPC22	
		SPC25		SPC25	
		SPTLC2		SPTLC2	
		stearoyl-CoA desaturase		stearoyl-CoA desaturase	
		STT3		STT3	
		TMP21		TMP21	
		VLCAD		VLCAD	
		Wolframin		Wolframin	
		YME1L1		YME1L1	
PTK7- complex	PTK7	APP	APP		
		BRI		BRI	
		CELSR2		CELSR2	
		DLK1		DLK1	
		FADS2		FADS2	
		HIFPH3/EGLN3		HIFPH3/EGLN3	
		ITM2C		ITM2C	

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		Nap1-like		Nap1-like	
		Reelin		Reelin	

TABLE 2

INDIVIDUAL PROTEINS OF THE COMPLEXES

Aph-1a	1	IPI00059964.1	28996
JUP	2	IPI00028128.1	81498
Psen1	3	IPI00028077.1	52668
ACAT1	4	IPI00019898.3	64833
BRI	5	IPI00031821.1	30338
calsyntenin 1	6	IPI00218869.1	108670
DLK1	7	IPI00218210.1	32910
DSCD75	8	IPI00010292.1	23865
Nicastrin	9	IPI00021983.1	78411
Pen-2	10	IPI00020516.1	12029
FACL3	11	IPI00031397.1	80346
FLJ10579	12	IPI00018730.1	52118
ITM2C	13	IPI00016014.1	30224
Presenilin 1	14	IPI00026333.1	52163
Sortilin 1	15	IPI00016022.1	92100
ITPR1	16	IPI00216955.1	314758
KiDins220	17	IPI00033429.1	197211
MDR1	18	IPI00027481.1	141463
Neurotrypsin	19	IPI00011063.2	97067
PLD3	20	IPI00163951.2	49573
RetSDR2	21	IPI00008260.1	32964
APLP2	22	IPI00031030.1	86956
APP	23	IPI00006608.1	86943
SFXN1	24	IPI00009368.2	35619
SORL1	25	IPI00022608.1	248441
SPC18	26	IPI00104128.1	20625
SPC22	27	IPI00030262.2	20253
SPC25	28	IPI00220125.1	25692
stearoyl-CoA desaturase	29	IPI00013007.2	41523

TMP21	30	IPI00028055.1	24976
VLCAD	31	IPI00163655.1	68788
YME1L1	32	IPI00099529.1	79832
LAPTM4B	33	IPI00020093.1	31735
S100alpha	34	IPI00220412.1	10546
Cadherin EGF LAG seven-pass G-type receptor 2	35	IPI00015346.1	317453
Calsyntenin 1	36	IPI00007257.1	109793
visinin-like 1	37	IPI00216313.1	22142
BACE1	38	IPI00216211.1	48212
CELSR2	39	IPI00015346.1	317453
FADS2 (delta-6-desaturase)	40	IPI00183786.1	52259
NogoA	41	IPI00219209.1	106360
OS-9	42	IPI00218476.1	76295
PDGFRB	43	IPI00015902.2	124093
PTK7	44	IPI00219694.1	118392
UGCGL1	45	IPI00024466.1	177190
CtnnB1	46	IPI00017292.1	
CtnnA1	47	IPI00215948.1	102776
CtnnA2	48	IPI00030907.1	105282
CtnnD1	49	IPI00182469.2	107349
NCadh	50	IPI00015717.1	99851
Reelin	51	IPI00021018.1	388402
Sortilin-related receptor	52	IPI00022608.1	248441
18 kDa microsomal signal peptidase subunit	53	IPI00104128.1	20625
CLGN	54	IPI00183309.1	73577
ECSIT	55	IPI00106506.1	49148
FLJ20342	56	IPI00015713.1	65084
KIAA0090	57	IPI00160376.1	111759
NICE-3	58	IPI00032413.1	28779
CK2B	59	IPI00010865.1	24942
PTP LOC114971	60	IPI00174190.1	22844

STT3	61	IPI00102885.1	80530
NicAChRa3	62	IPI00007259.1	55637
SLC4A2	63	IPI00337431.3	137009
HIFPH3/EGLN3	64	IPI00004971.1	52259
STX10	65	IPI00012264.2	28114
Presenilin 2	66	IPI00028485.1	50140
Wolframin	67	IPI00008711.1	100306
BACE1	68	IPI00011518.1	55764
FLJ30668	69	IPI00043733.1	33338
BSCv protein	70	IPI00031131.1	46480
FLJ39249	71	IPI00167501.1	27459
CGI-13	72	IPI00008847.1	52917
ITCH	73	IPI00061780.1	102803
Casein kinase II beta chain	74	IPI00010865.1	24942
Cathepsin B	75	IPI00013478.1	37808
Delta-6 fatty acid desaturase (FADS2)	76	IPI00003544.1	52259
Nogo-A	77	IPI00021766.3	129931
PDGFRB	78	IPI00015902.1	123968
ENSG00000144840	79	IPI00102897.1	26308
PTK7	80	IPI00012719.1	118260
FLJ13977	81	IPI00025520.1	53482
FLJ20481	82	IPI00016418.1	47655
SERPINA1	83	IPI00032180.1	46737
FLJ22390	84	IPI00009343.1	17098
SIM TO Y71H10A. 2.P.	85	IPI00170775.1	68184
Hypothetical protein tyrosine phosphatase ensg00000149185	86	IPI00102935.1	22844
ICAM-2	87	IPI00009477.1	30653
KIAA1181	88	IPI00003635.1	36879
KIAA1533	89	IPI00001841.1	72964
kinectin 1 (kinesin receptor)	90	IPI00032968.1	156093
Mesenchymal stem cell protein DSCD75	91	IPI00010292.1	23865
Neurotrypsin	92	IPI00011063.1	97012

PP1, regulatory subunit 15B	93	IPI00045837.1	79125
Protein amplified in osteosarcoma (OS-9)	94	IPI00013268.1	75562
Protein similar to stromal cell-derived factor 2	95	IPI00034198.1	23026
Protocadherin beta 8	96	IPI00009033.1	87624
REP8 protein	97	IPI00010353.1	30541
RING finger protein 5	98	IPI00012608.1	19881
Retinal short-chain dehydrogenase/reductase retSDR2	99	IPI00008260.1	32964
Stromal cell-derived factor 2-like 1	100	IPI00106642.2	23511
Thioredoxin domain-containing protein	101	IPI00001028.1	32535
Voltage-dependent anion channel 1	102	IPI00010430.1	30641
ATP-binding cassette, sub-family A member 3	103	IPI00017800.1	191388
CAMK4	104	IPI00002921.1	51926
KIAA0363	105	IPI00004538.1	156999
DCTN1	106	IPI00011446.1	127404
KIAA1250	107	IPI00033429.1	197211
FACL3	108	IPI00031397.1	80346
FACL4	109	IPI00029737.1	79188
KIAA0095	110	IPI00005680.1	93488
KIAA0922	111	IPI00021671.1	138688
PAS domain containing serine/threonine kinase	112	IPI00141040.1	142859
homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)	113	IPI00063544.1	33834
Integral membrane transporter protein	114	IPI00020093.1	31735
GPR49	115	IPI00021131.1	99998
NAP-1 related protein/NAP-1-like protein	116	IPI00155244.1	44159
SPTLC2	117	IPI00005751.1	62924
Delta-like homolog	118	IPI00009191.1	41143
25 kDa microsomal signal peptidase subunit	119	IPI00014148.1	25003

APP-C99	120		11278
Psen2	121	IPI00028485.1	50140

TABLE 3

BIOCHEMICAL ACTIVITIES OF THE COMPLEXES

Name of Complex	Biochemical activity
Nicastrin-complex	Gamma-secretase activity and assembly (trafficking)
Bace1-complex	APP processing beta-secretase
Psen-2-complex	Gamma-secretase activity
PTK7-complex	Role in neuronal signal transduction; involved in neural development and structural plasticity of the CNS; modulator of BACE function.

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

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CLAIMS

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
2. A protein complex comprising a first protein selected from the proteins listed in table 1, second column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm

DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

3. A protein complex comprising the proteins selected from the proteins in table 1, third column or a homologue thereof, or a variant thereof or functionally active fragments or functionally active derivatives of said proteins, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions;
 wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, but 1 to the number of proteins listed in table 1, fifth column of said complex, or a homologue or a variant thereof, or a functionally active fragment or functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins of said fifth column under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

5. The complex of any of claims 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of claim 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of claims 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of claims 1 - 7 that is involved in the biochemical activity as stated in table 3.
9. A process for preparing a complex of any of claims 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to claim 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of claims 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of claims 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a

functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

14. Nucleic acid encoding a protein according to claim 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to claim 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to claim 1 (a) and at least one of said proteins, being selected from the second group of proteins according to claim 1 (b).
16. Host cell, containing a vector comprising at least one of the nucleic acid of claim 14 and /or a construct of claim 15 or containing several vectors each comprising at least the nucleic acid encoding at least one protein selected from the first group of proteins according to claim 1 (a) and the nucleic acid encoding at least one protein selected from the second group of proteins according to claim 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, which binds the complex of any of claims 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and/or an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the group of proteins according to claim 13.

18. A kit comprising in one or more containers the complex of any of claims 1 - 8 and/or the proteins of claim 13, optionally together with an antibody according to claim 17 and/or further components such as reagents and working instructions.
19. The kit according to claim 18 for processing a substrate of a complex of any one of claims 1 - 8.
20. The kit according to claim 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
21. Array in which at least a complex according to any of claims 1 - 8 and/or at least one protein according to claim 13 and/or at least one antibody according to claim 17 is attached to a solid carrier.
22. A process for processing a substrate of a complex of any one of claims 1 - 8 comprising the step of bringing into contact a complex to any of claims 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of claims 1 - 8 and/or any of the proteins according to claim 13.
24. A pharmaceutical composition according to claim 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
25. A method for screening for a molecule that binds to the complex of any one of claims 1 - 8 and/or any of the proteins of claim 13, comprising the following steps:
 - (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of claims 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.
27. The method of claim 26, wherein the amount of said complex is determined.
28. The method of claim 26, wherein the activity of said complex is determined.
29. The method of claim 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of claim 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of claim 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of claims 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of claims 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of claims 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the claims 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample

from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of claim 35, wherein the amount of said complex is determined.
37. The method of claim 35, wherein the activity of said complex is determined.
38. The method of claim 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of claim 35, wherein the amount of the individual protein components of said complex are determined.
40. The method of claim 39, wherein said determining step comprises determining whether any of the proteins according to claim 13 is present in the complex.
41. The complex of any one of claims 1 - 8, or proteins of claim 13 or the antibody or fragment of claim 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of claims 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.
43. The method according to claim 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to claim 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of claims 1 - 8 and/or any of the proteins listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

FIGURE 1

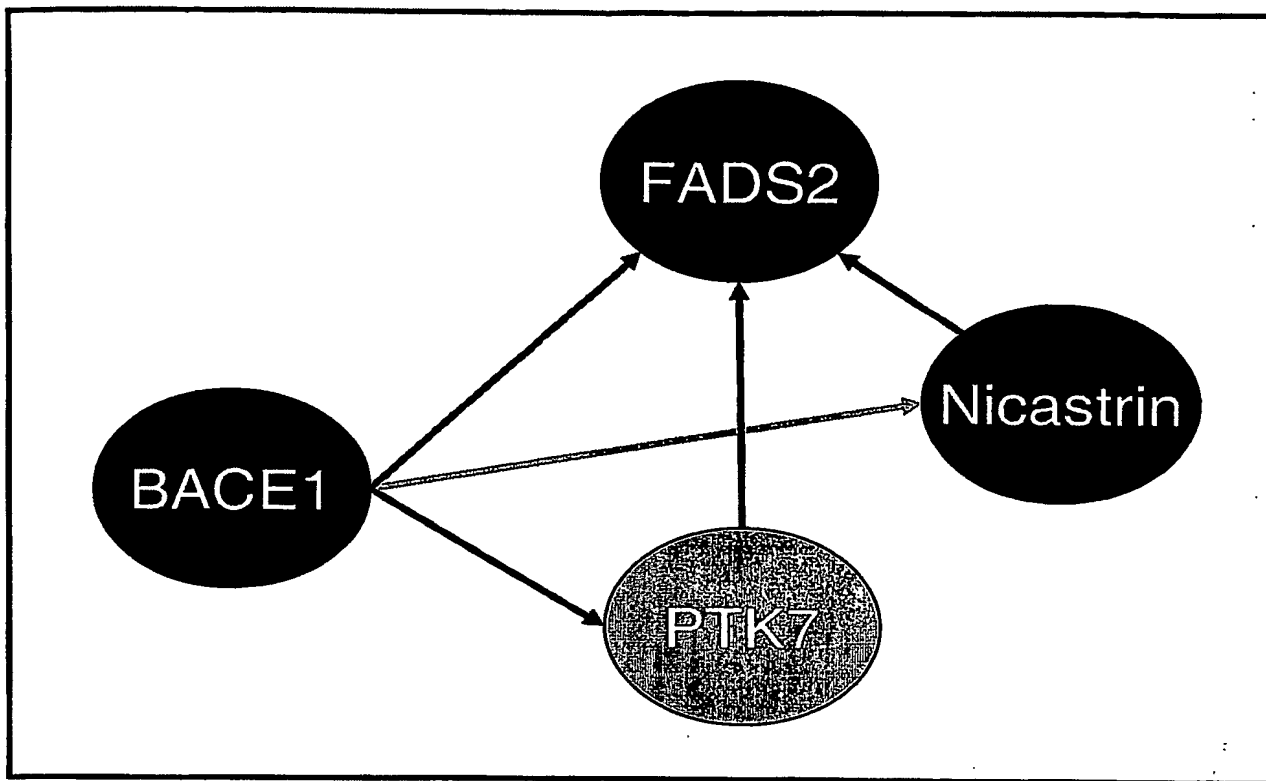


FIGURE 2

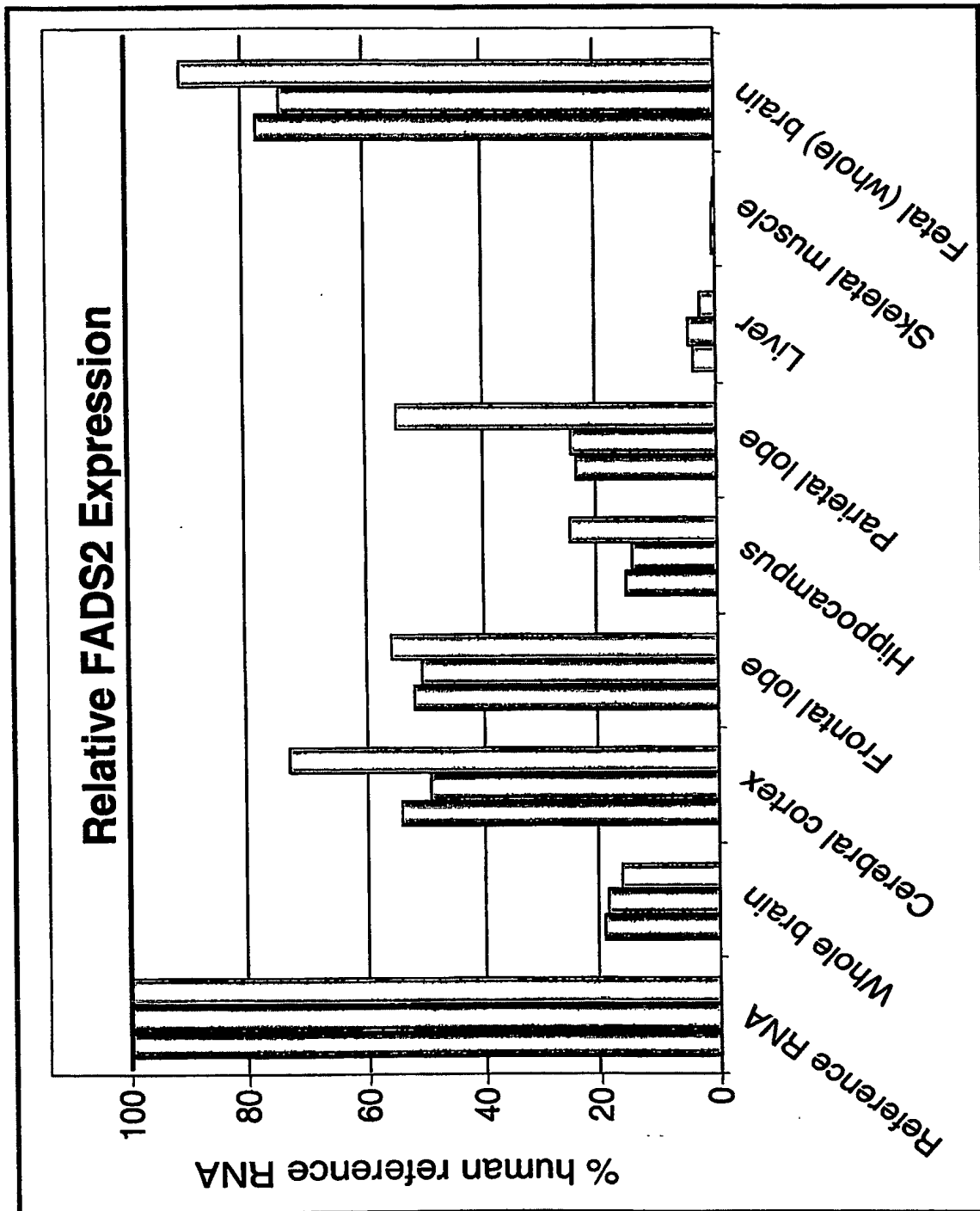


FIGURE 3 A

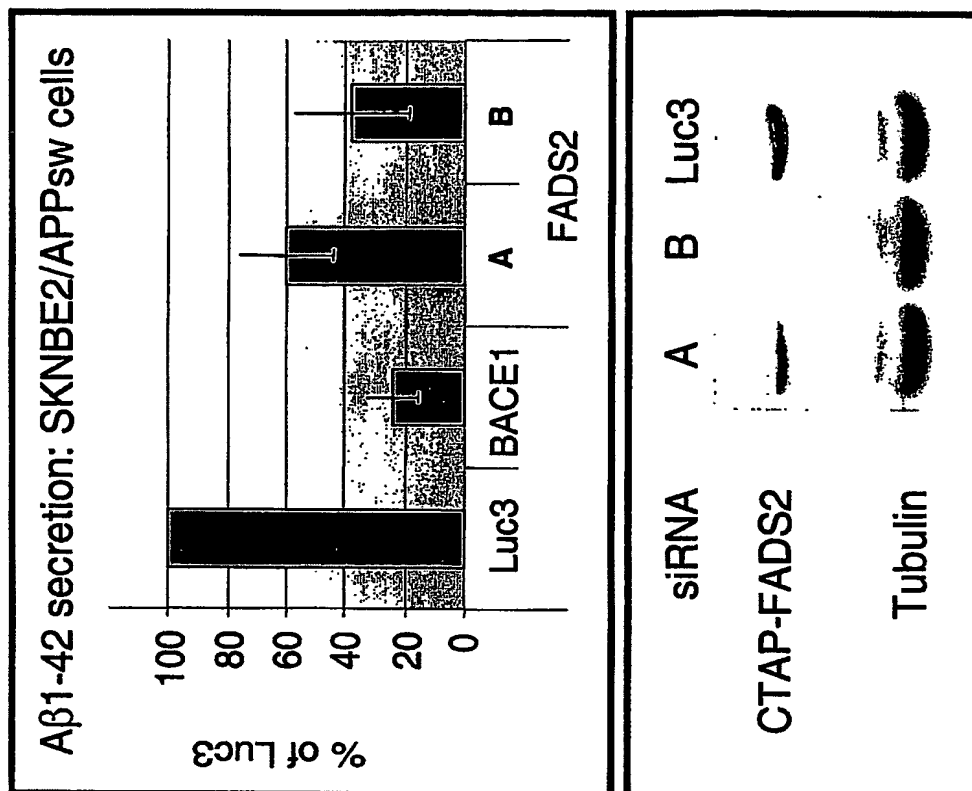


FIGURE 3 B

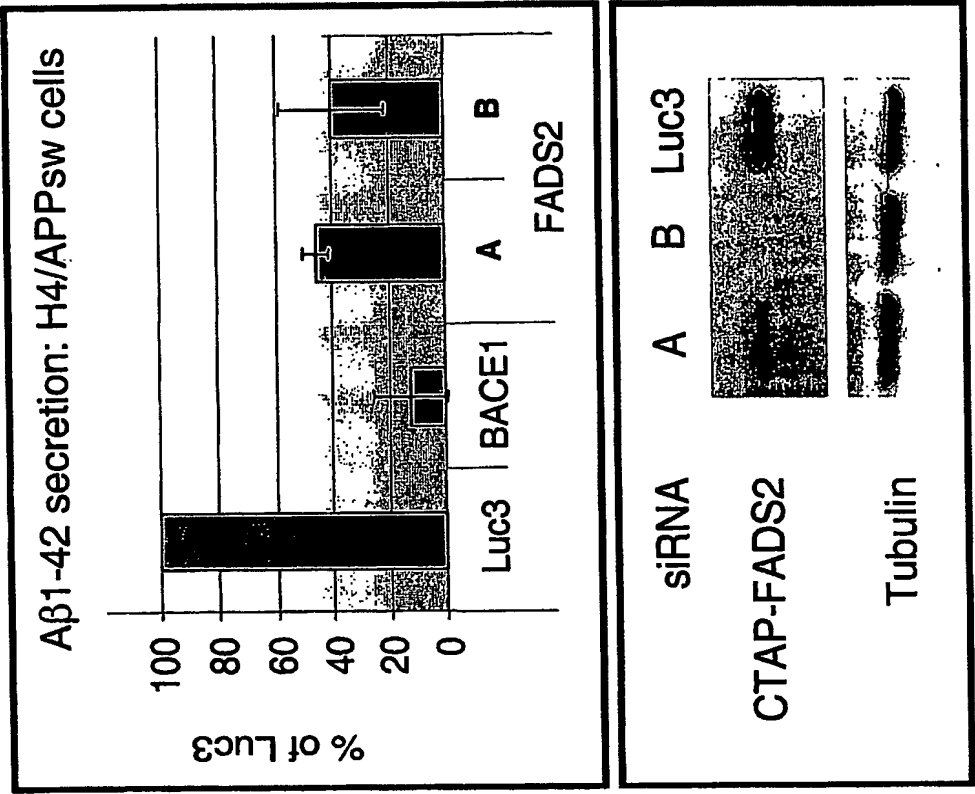


FIGURE 4

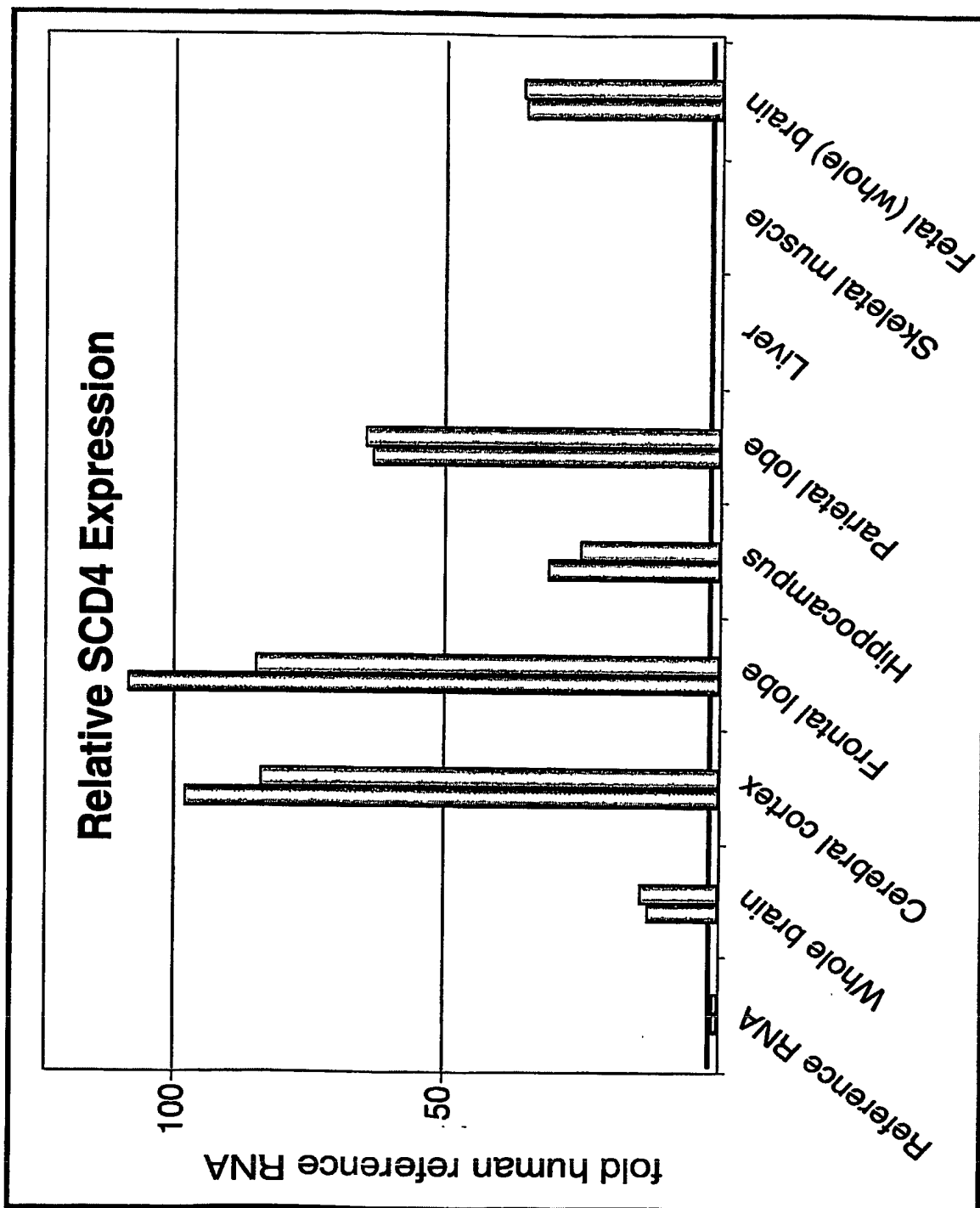


FIGURE 5

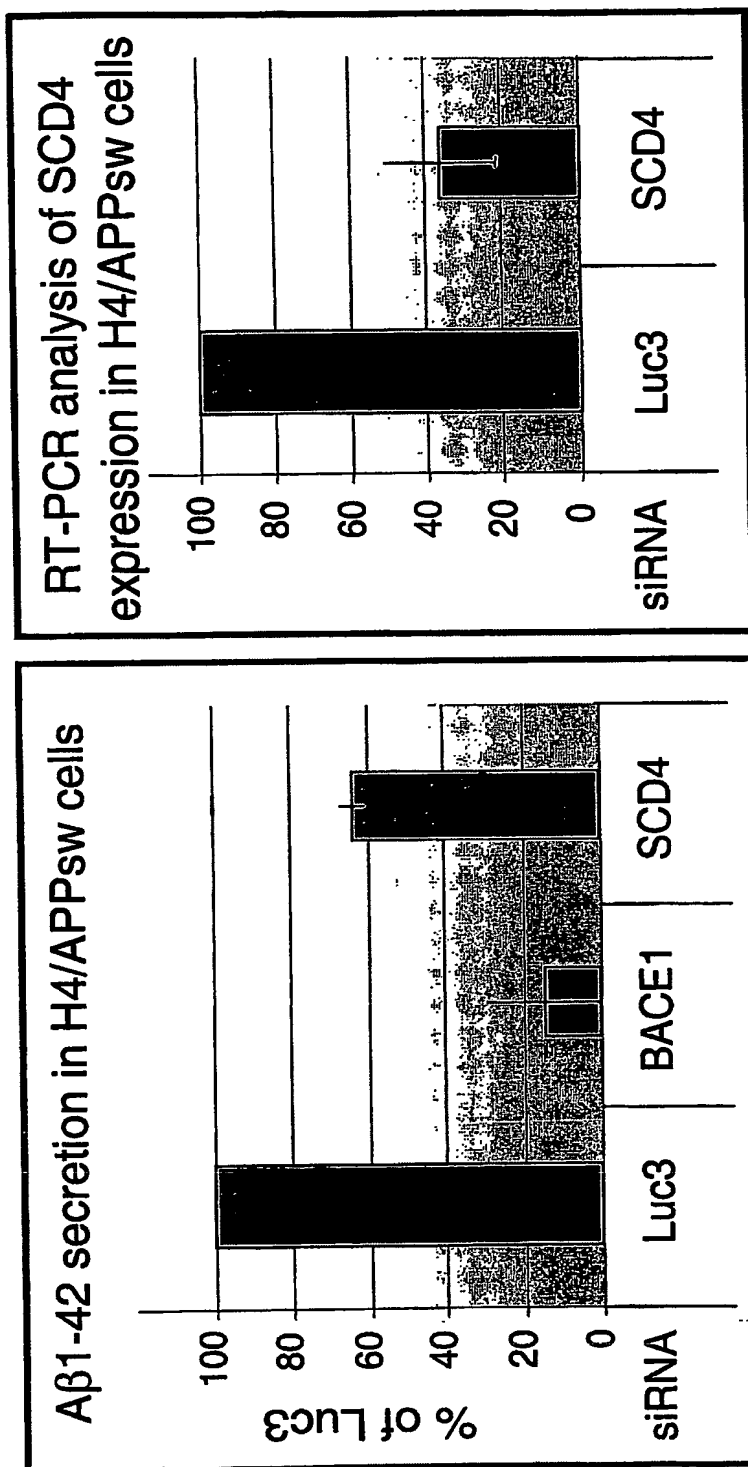


FIGURE 6

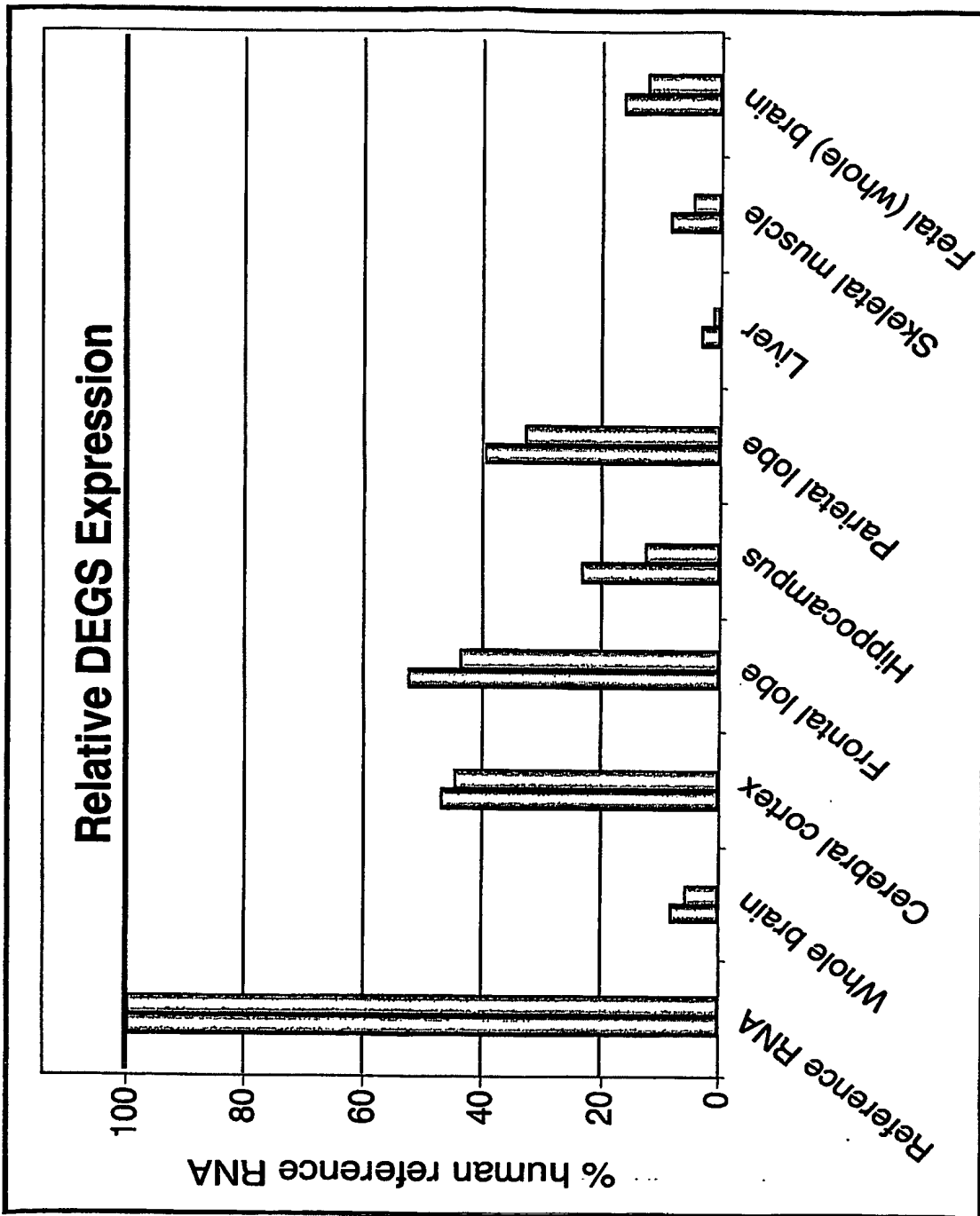
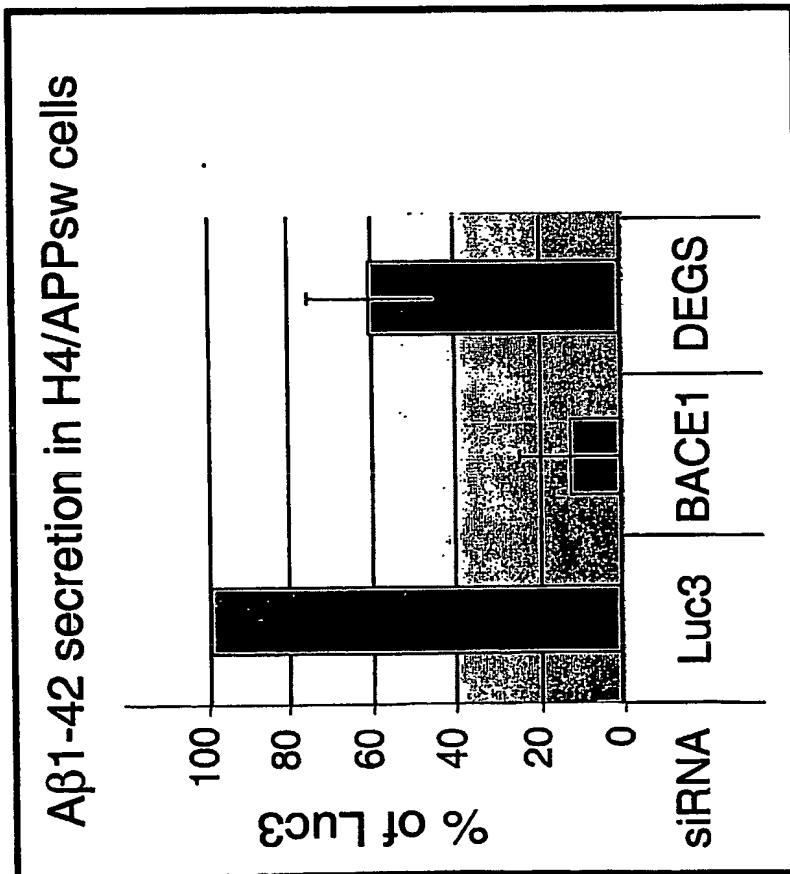
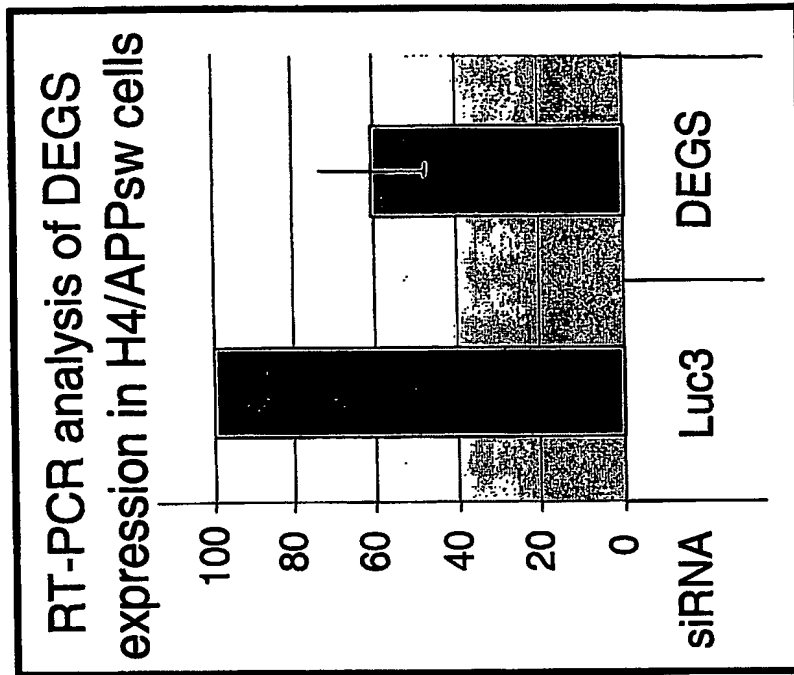


FIGURE 7



SEQUENCES

SEQ ID No:1 (Aph-1a)

MGA AVFFGCTFVAFGPAFALFLITVAGDPLRVILVAGAFFWLVSLLLASVWVFILVHVTD
RSDARLQYGLLIFGA AVSVLLQE VFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVS
GLSFGIISGVFSVINILADALGPGVVG I HG DSPYYFLTSAFLTAA ILLHTFWGVVFFDACE
RRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSL
LCRRQEDSRVMVYSALRIPPED

SEQ ID No: 2 (JUP)

EVMNLMEQPIKVTEWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKT
TYTQGVPPSQGDLEYQMSTTARAKRVREAMCPGVSGEGQLALLATQVEGQATNLQRL
AEP S QLLKSAIVHLINYQDDAELVTRALPELTKLLNDEDPVVVTKAAMIVNQLSKKEASRR
ALMGSPQLVA AVVRTMQNTSDLD TARCTTSILHNLSHHREGLLAIFKSGGIPALVRMLSS
PVESVLFYAITTLHNLLLYQEGAKMACAGRRRAQKMVPLLNNKNNPKFLAITTDCLQLLAYG
NQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVL SVCPSNKP AIVEAGGMQALG
KHLTSNSPRLVQNCLWTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLT CATGTLSN
LTCNNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPEAEMAQNSVR
LNYGIPAIVKLLNQPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDA
QRHVAAGTQQPYTDGVRMEEIVEGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSV
ENIQRVAAGVLC ELAQDKEAADAIDAEGASAPLMELLHSRNEG TATYAAAVLFRISEDKN
PDYRKRVSVELTNSL FKHDPAAWEAAQSMIPINEPYGDDMDATYRPMYSSDVPLDPLE
MHMDMDGDYPIDTYS DGLRPPYPTADHMLA

SEQ ID No: 3 (Psen1)

MTELPAPLSYFQNAQMSEDNHLSENTVRSQNDNRERQEHNDRRLGHPEPLSNGRPQ
GNSRQVVEQDEEEDEELTKYGA KHVIMLFVPVTL CMVVVVATIKSVSFYTRKDGQLIYT
PFTEDTETVGQRALHSILNAAIMISVIVMTILLV VLYKYRCYKVIHAWLISSLLLLFFFSFIY
LGEVFKTYNVAVDYITVALLIWNFGVVGMI SIHWKGPLRLQQAYLIMISALMALVFIKYLPE
WTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGD
PEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEWEAQRD SHLGPHRSTPESRA
AVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL
TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI

SEQ ID No: 4 (ACAT1)

MVGEEKMSLRNRLSKSRENPEEDEDQRNPAKESLETSPNGRIDIKQLIAKKIKLTAEAEA
 RLKPFFMKEVGSHFDDFVTNLIKESASLDNGGCALTTFVLEGEKNNHRAKDLRAPPEQ
 GKIFIARRSLLDELLEVDHIRTIIYHMFIALILFILSTLVVDYIDEGRLVLEFSLLSYAFGKFPT
 VVWTWWIMFLSTFSVPYFLFQHWATGYSSSHPLIRSLFHGFLFMIFQIGVLGFGPTYV
 VLAYTLPPASRFIIIFEQIRFVMKAHSFVRENVPRVLNSAKEKSSTVPIPTVNQYLYFLFAP
 TLIYRDSYPRNPTVRWGYVAMKFAQVFGCFFYVYYIFERLCAPLFRNIKQEPFSARVLVL
 CVFNSILPGVLILFLTFFAFLHCWLNAFAEMLRFGDRMFYKDWWNSTSYSNYRTWNV
 VVHDWLYYYAYKDFLWFFSKRFKSAAMLAVFAVSAVVHEYALAVCLSFFYPVLFVLFMF
 FGMAFNFIVNDSRKKPIWNVLMWTSFLGNGVLLCFYSQEWYARQHCPLKNPTFLDYV
 RPRSWTCRYVF

SEQ ID No: 5 (BRI)

MVKVTFNSALAQKEAKKDEPKSGEEALIIPDAVAVDCKDPDDVVPVGQRRRAWCWCM
 CFGLAFLMAGVILGGAYLYKYFALQPDDVYYCGIKYIKDDVILNEPSADAPAALYQTIEENI
 KIFEEEEVEFISVPVPEFADSDPANIVHDFNKKLTAYLDLNLDKCYVIPLNTSIVMPPRNL
 ELLINIKAGTYLPQSYLIHEHMOVITDRIENIDHLGFFIYRLCHDKETYKLQRRETIKGIQKRE
 ASNCFAIRHFENKFAVETLICS

SEQ ID No: 6 (calsyntenin 1)

MLRRPAPALAPAARLLLGLLGGGVWAARVNHKHPWLEPTYHGIVTENDNTVLLDPP
 LIALDKDAPLRFAGEICGFKIHGQNVPFDAVVVDKSTGEGVIRSKEKLDCELQKDYSFTIQ
 AYDCGKGPDGTNVKKSHKATVHIQVNDVNEYAPVFKEKSYKATVIEGKQYDSILRVEAV
 DADCSPQFSQICSYEIITPDVPFTVDKDGYYIKNTEKLNYGKEHQYKLTVTAYDCGKKRAT
 EDVLVKISIKPTCTPGWQGWNNRIEYEPGTGALAVFPNIHLETCDPVASVQATVELETS
 HIGKGCDRDTYSEKSLHRLCGAAAGTAELLPSPSGSLNWTMGLPTDNGHDSQVFEFN
 GTQAVRIPDGVVSVSPKEPFTISVWMRHGPFGRKKETILCSSDKTDMNRHHYSLYVHG
 CRLIFLFRQDPSEEKKYRPAEFHWKLNQVCDEEWHHYVLNVEFPSVTLYADGTSHEPF
 SVTEDYPLHPSKIETQLVVGACWQEFSGVENDNETEPVTVACAGGDLHMTQFFRGNLA
 GLTLRSGKLADKKVIDCLYTCKEGLDLQVLEDSEGRGVQIQAHRSQVLTLLEGEDLGELD
 KAMQHISYLNRSRQFPTPGIRRLKITSTIKCFNEATCISVPPVDGYVMVLQPEEPKISLSGV
 HHFARAASEFESSEGVFLFPELRIISTITREVEPEGDGAEDPTVQESLVSEEIVHDLDTC
 VTVEGEELNHEQESLEVDMARLQQKGIEVSSSELGMTFTGVDTMASYEEVLHLLRYRN
 WHARSLDRKFKLICSELNGRYISNEFKVEVNVIIHTANPMEHANHMAAQPFVHPEHRS

FVDLSGHNLANPHFPAVVHSTATVIVVCVSSLVFMILGVFRIRAAHRRRTMRDQDTGKE
NEMDWDDSAITITVNPMEYEDQHSSEEEEEEEEEEESEDGEEEDDITSAESESSEEE
EGEQGDPQNATRQQQLEWDDSTLSY

SEQ ID No: 7 (DLK1)

MTATEALLRVLLLLLAFGHSTYGAECFPACNPQNGFCEDDNVCRCQPGWQGPLCDQC
VTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRACSSAPCANNGTCVSLDGGLYECS
CAPGYSGKDCQKKDGPCVINGSPCQHGGTCVDDEGRASHASCLCPPGFSGNFCEIVA
NSCTPNPCENDGVCTDIGGDFRCRCPCAGFIDKTCSPVTNCASSPCQNGGTCLQHTQ
GQAICFTILGVLTSLVVLGTVGIVFLNKCETWVSNLRYNHMLRKKKNLLLQYNSGEDLAV
NIIFPEKIDMTTFSKEAGDEEI

SEQ ID No: 8 (DSCD75)

MLGLLVALLALGLAVFALLDVWYLVRLPCAVLRARLLQPRVRDLLAEQRFPGRVLPSDL
DLLLHMNNARYLREADFARVAHLTRCGVLGALRELRAHTVLAASCARHRRSLRLLPEFE
VRTRLLGWDDRAFYLEARFVSLRDGFVCALLRFRQHLLGTSPERVVQHLCCRRVEPPE
LPADLQHWISYNEASSQLLRMESGLSDVTKDQ

SEQ ID No:9 (Nicastrin)

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
GCQSSISGDTGVIHVVEKEEDLQWVLTGPNPPYMVLLSKHFTRDLMEKLGRTSRIA
GLAVSLTKPSPASGFSPSVQCPNDGFGVYSNSYGPFAHCREIQWNSLGNGLAYEDFS
FPIFLEDENETKVIKQCYQDHNLSQNGSAPTFLCAMQLFSHMHAVISTATCMRRSSIQ
STFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDRVRVVAATRLDSRSFFWNVAPGAE
SAVASFVTQLAAAEALQKAPDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPV
QLENVDSFVELGQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVIL
RRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYYQSIYDTAENINVSYPEWLS
PEEDLNFVTDATAKALADVATVLGRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKANNS
WFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVVQYALANLTGTVVNLTREQCQDPSK
VPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARALSPAFELSQWSSTEYSTWT
ESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGAVSY

SEQ ID No:10 (Pen-2)

MNLERVSNEEKLNLCKRYYLGGFAFLPFLWLNVNIFWFFREAFVLPAYTEQSQIKGYVWR
SAVGFLFWVIVLTSWITIFQIYRPRWGALGDYLSFTIPLGTP

SEQ ID No: 11 (FACL3)

MNNHVSSKPSMTMLKHTINPILLYFIHFLISLYTILTYIPFYFFSESQRQESNRKAKPVNSK
PDSAYRSVNSLDGLASVLYPGCDTLDKVFTYAKNFKKNRLLGTREVLNEEDEVPNG
KIFKKVILGQYNWLSYEDVVFVRAFNFNGNLQMLGQKPKTNIAIFCETRAEWMIAAQACF
MYNFQLVTLYATLGGAIVHALNETEVTNIITSKELLQTKLKDIVSLVPRLRHITVDGKPPT
WSDFPKGIIVHTMAAVEALGAKASMENQPHSKPLPSDIIVIMYTSGSTGLPKGVMISHS
NIIAGITGMAERIPELGEEDVYIGYLPLAHVLELSAELVCLSHGCRIGYSSPQTLADQSSKI
KKGSKGDTSMKPTLMAAVPEIMDRIYKNVMNKVSEMSSFQRNLFILAYNYKMEQISKG
RNTPLCDSFVFRKVRSLGGINRLLCGGAPLSATTQRFMNICFCPPVGQGYGLTESAG
AGTISEVWDYNTGRVGAPLVCCEIKLNWEEGGYFNTDKPHPRGEILIGGQSVTMGGY
KNEAKTKADFSSEDENGQRWLCTGDIGEFEPDGCLKIIDRKKDLVKLQAGEYVSLGKVEA
ALKNLPLVDNICAYANSYHSYVIGFVVPNQKELTELARKKGLKGTWEELCNCEMENEV
LKVLEAAISASLEKFEIPVKIRLSPEPWTPETGLVTDFAFLKRKELKTHYQADIERMYGR
K

SEQ ID No: 12 (FLJ10579)

MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTS
DPGRHVMLLRAPVGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSL
RGLAGEIVGEVRCHMEENQRRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESE
GGYTTANAESDNERDSDKESEDGEDEVSCETVKMGRKDSLDLEEEAASGASSALEAG
GSSGLEDLVPLLQQADELHRGDEQKGREGFQLLLNNKLVDYGSQRQDFLWRLARAYSMD
CELTEEVSEKKSIALDGKEEAEEALEKGDESADCHLWYAVLCGQLAEHESIQRRIQSGF
SFKEHVDKAIALQPENPMAHFLLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQS
FLKAEELQPGFSKAGRVYISKCYRELGKNSEARWWMKLLELPDVTKEDLAIQKDLEEL
EVILRD

SEQ ID No: 13 (ITM2C)

MVKISFQPAVAGIKGDKADKASASAPASATEILLTPAREEQPPQHRSKRGGSVGGVC
YLSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVVRTQMELEEDV
KIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTIVLPPRNF

WELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRRRATRRRI
NKRGAKNONAIRHFENTFVVETLICGVV

SEQ ID No:14 (Presenilin)

MTelpAPLSYFQNAQMSEDNHLsNTNDNRERQEHNDRRLGHPEPLSNGRPQGNSR
QVVEQDEEEDEELTKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE
DTETVGQRALHSILNAAIMISVIVVMTILLVVLKYRCYKVIHAWLISSLLLLFFFSFIYLGE
VFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWT
AWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEA
QRRVSKNSKYNAESTERESQDTVAENDDGGFSEWEAQRDShLGPHRSTPESRAAV
QELSSSILAGEDPEERGVLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTLL
LLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI

SEQ ID No:15 (Sortilin/Sort1)

MERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRLDAPPPAAPLPRWSGPIGVS
WGLRAAAAGGAFPRGGRWRRSAPGEDEECGRVRDFVAKLANNTHQHVFDDLGRGSVS
LSWVGdstGVILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIRTEFGMAI
GPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTDLPFHPLTQMMYSPQNSDYLLA
LSTENGLWVSKNFGGKWEEIHKAVCLAKWGSdNTIFFTTYANGSCKADLGALELWRTS
DLGKSFKTIGVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDtWSMAQLPSVGQE
QFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYSKSLDRHLYTTTGGETDFTNV
TSLRGVYITSVLSEDNSIQTMITFDQGGRWTHLRKPENSECDATAKNKNECSLHIHASYS
ISQKLNVPMAPLSEPNAVGIviaHGSVGDaisVMVPDVYISDDGGYSWTKMLEGPHYTYI
LDSGGIIVaIEHSSRPINVIKfSTDEGQCWQTYTfTRDPIYFTGLASEPGARSMNISIWGF
TESFLTSQWVSYTIDFKDILERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKS
SMCQNGRDYVVTkQPSICLCSLEDfLCDFGYRpendSKCveQPELKGHDLEfCLYGR
EEHLTTNGYRKIPGDKCQGGVNPVREVkdLKKKCTSNFLSPEKQNSKSNsVPIILAIVGL
MLVTVVAGVLIVKKYVCGGRFLVhrySVLQQHAEANGVDGVDALDTASHTNKSGYHDD
SDEDLLE

SEQ ID No: 16 (ITPR1)

MSDKMSSFLHIGDICSlyAEGSTNGFISTLGLVDDRCVVQPETGDLNNPPKKFRDCLFK
LCPMNRYSaQKQFWKAaKPGANSTTDaVLLNKLHHAADLEKKQNETENRKLlGTVIQY
GNVIQLLHLKSNKYLTvNKRLPALLEKNAMRVTLDEAGNEGSWFYIQPFYKLRSIGDSVV

IGDKVVLNPVNAGQPLHASSHQLVDNPGCNEVNSVNCNTSWKIVLFMKWSDNKDDILK
 GGDVVRLEFHAEEQEKFLTCDEHRKKQHVFRLRTTGRQSATSATSSKALWEVEVVQHDPC
 RGGAGYWNSLFRFKHLATGHYLA AEVDPDFEEECLEFQPSVDPDQDASRSRLRNAQE
 KMOVSLVSVPEGNDISSIFELDPPTLRGGDSLVPNRNSYVRLRHLCNTNTWVHSTNIPIDKE
 EEKPVMLKIGTSPVKEDKEAFAIVPVSPA EVRDLDFANDASKVLGSIAGKLEKGTITQNE
 RRSVTKLLEDLVYFVTGGTNSGQDVLEVVFSPKPNRERQKLMREQNILKQIFKLLQAPFT
 DCGDGPMLRLEELGDQRHAPFRHICRLCYRVL RHSSQQDYRKNQEYIAKQFGFMQKQIG
 YDVLAE DTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREPRFLDYLS DLCVSMNKSIPVT
 QELICKAVLNPTNADIL IETKLVL SRFEFEGVSSTGENALEAGEDEEEVWLFWRDSNKEI
 RSKSVRELAQDAKEGQKEDRDVLSYYRYQLNLFARMCLDRQYLAIN EISGQLDVDLILR
 CMSDENLPYDLRASFCRLMLMHVDRDPQE QVTPVKYARLWSEIPSEIAIDDYDSSGA
 SKDEIKERFAQTMEFVEEYLRDVVCQRFPFSDKEKNKLTFEVVNLARNLIYFGFYNFSDL
 LRLTKILLAILDCVHVTTIFPISKMAKGEENKGNNDVEKLKSSNVMRSIHGVGELMTQVVL
 RGGGFLPMTPM AAPEGNVKQAEPEKEDIMVMDTKLKIIELQFILNVRLDYRISCLLCIFK
 REFDESNSQTSETSSGNSSQEGPSNVP GALDFEHIEEQAEGIFGGRKVYFHEENTPLDL
 DDHGGRTFLRVLLH LTMHDYPPLVSGALQLLFRHFSQRQEV LQAFKQVQLLVTSQDVD
 NYKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGENEHKKTEEGNNKPQKHES
 TSSYNRYRVVKEILIRLSKLCVQESASVRKSRKQQQRLLRNMG AHAVVLELLQIPYEKAED
 TKMQEIMRLAHEFLQNF CAGNQQNQALLHKHINLFLNPGILEAVTMQHIFMNNFQLCSEI
 NERVVQH FVHCIETHGRNVQYIKFLQTIVKAEGKFIKKCQDMVMAELVNSGEDVLVFN
 DRASFQTLIQMMR SERDRMDENSPLMYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIV
 RVVTHEDCIPEVKIAYINFLNH CYVDTEVEMKEIYTSNHMWKLFENFLVDICRACNNTSD
 RKHADSILEKYVTEIVMSIVTTFFSSPFS DQSTTLQTRQPVFVQLLQGVFRVYHCNWLMP
 SQKASVESCIRVLS DVAKSRAIAIPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARR
 DSVLAASRDYRNIIERLQDIVSALEDRLRPLVQAELSVLVDVLHRPELLFPENTDARRKC
 ESGGFICKLIKHTKQLLEENEEKLCIKVLQTLREMMTKDRGYGEKLISIDELDNAELPPAP
 DSENATEELEPSPPLRQLEDHKRGEALRQVLVNRYYG NVRPSGRRESLTSFGNGPLSA
 GGP GKPGGGGGGGSGSSSMSRGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVFHES
 ILLAIALLEG GNTTIQHSFFCRLTEDKKSEKFFKV FYDRMKVAQQEIKATVTVNTSDLGNK
 KKDDEVDRDAPSRKKAKEPTTQITEEVRDQ LLEASAATRKAFTTFRREADPD DHYQPG
 EGTQATADKAKDDLEMSAVITIMQPILRFLQLLCENHNRDLQNFLRCQNNKTNYNLVCE
 TLQFLDCICGSTTGGLGLLGLYINEKNVALINQTLESLTEY CQGPCHENQNCIATHESNGI
 DIITALILNDINPLGKKRMDLVLELKAKNASKLLLAIMESRHDSENAERILYNMRPKELVEVI
 KKAYMQGEVEFEDGENGEDGAASPRNVGHNIYILAHQLARHNKELQSMLKPGGQVDG

DEALEFYAKHTAQIEIVRLDRTMEQIVFPVPSICEFLTKE SKLRIYYTTERDEQGSKINDFF
 LRSEDLFNEMNWQKKLRAQPVLYWCARNMSFWSSISFNLA VLMNLLVAFFYPFKGV RG
 GTLEPHWSG LLWTAMLISLAIVIALPKPHGIRALIASTILRLIFSVGLQPTLFLLGAFNV CNK
 IIFLMSFVGNCGTFTTRGYRAMVLDVEFLYHLLYLVICAMGLFVHEFFYSLLLFDLVYREET
 LLNVIKSVTRNGRSIILTAVLALILVYLFSIVGYLFFKDDFILEVDRLPNETAVPETGESLAS
 EFLFSDVCRVESGENC SSPAPREELVPAEETE QDKEHTCETLLMCIVTVLSHGLRSGGG
 VGDVLRKPSKEEPLFAARVIYDLLFFFMVIII VLNLI FGVIIDTFADLRSEKQKKEEILKTTCFI
 CGLERDKFDNKTVTFEEHIKEEHNMWHYLCFIVLVKVKDSTEYTG PESYVAEMIKERNL
 DWFPRMRAMSLVSSDSEGEQNELRN LQEKLESTMKLV TNLSGQLSELKDQMTEQRKQ
 KQRIGLLGHPPHMNVNPQQPA

SEQ ID No: 17 (KiDins220)

LQLSVKMSVLISQSVINYVEEENIPALKALLEKCKDVDERNECGQTPLMIAAEQGNLEIVK
 ELIKNGANCNLEDLDNWTALISASKEGHVHIVEELLKCGVNLEHRDMGGWTALMWACY
 KGRTDVVELLLSHGANPSVTGLYSVYPIIWAAGRGHADIVHLLLQNGAKVNCSDKYGTT
 PLVWAARKGHLECVKHLLAMGADV DQEGANSMTALIVAVKGGYTQSVKEILKRNP NVN
 LTDKDGNTALMIASKEGHTEIVQDLLDAGTYVNIPDRSGDTV LIGAVRGGHVEIVRALLQ
 KYADIDIRGQDNKTALYWAVEKGNATMVRDILQCNPDTEICTK DGETPLIKATKMRNIEV
 VELLLDKGAKVSAVDKKGDTPLHIAIRGRSRKLAELLRNPKDGRLLYRPNKAGETPYNI
 DCSHQKSILTQIFGARHLSPTETDGDMLGYDLYSSALADILSEPTMQPPICVGLYAQWG
 SGKSFLLKKLEDEMKT FAGQQIEPLFQFSWLIVFLTLLLCGGLG LLFAFTVHPNLGIAVSL
 SFLALLYIFFIVIYFGGRREGESWNWAWVLSTRLARHIGYLELLLKLMFVNPPPELPEQTTK
 ALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREF GFLATRLFRVFKTEDTQGKKK
 WKKTCCLPSFVIFLFIIGCIISGITLLAIFRVDPKHLTVNAV LISIASVVGLAFVLNCR TWWQ
 VLDSSLNSQRKRLHNAASKLHKLKSEGFMKVLKCEVELMARM AKTIDSFTQNQTRLVVII
 DGLDACEQDKVLQMLD TVRVLF SKGPFIAIFASDPHIIKAINQNLNSVLRDSNINGHDYM
 RNIVHLPVFLNSRGLSNARKFLVTSATNGDVPCSDTTGIQEDADRRVSQNSLGEMTKLG
 SKTALNRRD TYRRRQMQR TITRQMSFDLTKLLVTE DWFS DISPQTMRRLLNIVSVTGRL
 LRANQISFNWDR LASWINLTEQWPYRTSWLILYLEETEGIPDQMTLKT IYERISKNIPTTK
 DVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKVFLPCTVNLDPK LREIIADVRAAREQISIG
 GLAYPPLPLHEGPPRAPSGYSQPPSVCSSTS FNNGPFAGGVVSPQPHSSYYSGMTGPQ
 HPFYNRPF FAPYLYTPRYYPGGSQHLSRPSVKTS LPRDQNNGLEVIKEDAAEGLSSPT
 DSSRGSGPAPGPV VLLNSLNVDACEK LKQIEGLDQSMLPQYCTTIKKANINGRVL AQC
 NIDELKKEMNMNFGDWHLFRSTVLEMRNAESHVVPEDPRFLSESSSGPAPHGEPARR

ASHNELPHTELSSQTPYTLNFSFEELNTLGLDEGAPRHSNLSWQSQTRRTPSLSSLNS
 QDSSIEISKLTDKVQAEYRDAYREYIAQMSQLEGGPGSTTISGRSSPHSTYYMGQSSSG
 GSIHSNLEQEKGKDSEPKPDDGRKSFLMKRGDVIDYSSSGVSTNDASPLDPITEEDEKS
 DQSGSKLLPGKKSSERSSLFQTDLKLKGSGRLRYQKLPSDEDESGTEESDNTPLLKDDK
 DRKAEGKVERVPKSPEHSAEPIRTFIKAKEYLSDALLDKKDSSDSGVRSSSESSPNHSLH
 NEVADDSQLEKANLIELEDDSHSGKRGIPHSLSGLQDPPIARMSICSEDKKSPSECSLIAS
 SPEENWPACQKAYNLNRTPSTVTLNNSAPANRANQNFDEMEGIRETSQVILRPSSSP
 NPTTIQENENLKSMT HKRSQRSSYTRL SKDPPELHAAASSESTGFGEERESIL

SEQ ID No: 18 (MDR1)

MDLEGDRNGGAKKKNNFFKLNNKSEKDKKEKKPTVSVFSMFRYSNWLDKLYMVVGTLA
 AIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMNLEEDMTRYAYY
 YSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGEINTRLTD
 DVSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLT LVILAISPV LGLSAAVWAKILSSF
 TDKELLAYAKAGAVAEVLA AIRT VIAFGGQK KELERYNKNLEEAKRIGIKKAITANISIGA
 AFLLIYASYALAFWYGTTLVLSGEYSIGQVLT VFFSVLIGAFSVGQASPSIEAFANARGAA
 YEIFKIIDNKPSIDSYSGHKKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSGQTV
 ALVGNSGCGKSTTVQLMQRLYDPTEGMVSVDGQDIRTINVRFLREIIGVVSQEPVLFATT
 IAENIRYGRENVMTMDEIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIAR
 ALVRNPKILLLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAGFDDG
 VIVEKGNHDELMKEKGIYFKLVTMQTAGNEVELENAADESKSEIDALEMSSNDSRSSLIR
 KRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTWPYFVVGVFCAIINGG
 LQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLFLALGIISFITFFLQGFTFGKAGEILTKRL
 RYMVFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNIANLGTGII
 ISFIYGWQLTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGAGKIAIEAENFRTVVSLT
 QEQKFEHMYAQSLQVPYRNSLRKAHIFGITFSFTQAMMYFSYAGCFRFGAYLVAHKLM
 SFEDVLLVFSVAVFGAMAVGQVSSFAPDYAKAKISAAHIIMIEKTPLIDSYSTEGLMPNTL
 EGNVTFGEVVFNYPTRPDIPVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERFYDPL
 AGKVLLDGKEIKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNSRVVSQEEIVRAAKE
 ANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHILLLDEATSALDTESEK
 VVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSMVS
 VQAGTKRQ

SEQ ID No: 19 (Neurotrypsin)

MTLARFVLALMLGALPEVVGFDSVLNDSLHSHRHSPAGPHYPPYLPTQQRPPRTRP
 PPPLPRFPRPPRALPAQRPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLRWAE
 VPPFLERSPPASWAQLRGQRHNFCSRSPDGAGRPWCFYGDARGKVDWGYCDCRHGS
 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIKQTPFSG
 LGLPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCSFSHGPTFPIIRLAGGS
 SVHEGRVELYHAGQWGTVCDDQWDDADADEVICRQLGLSGIAKAWHQAYFGEGSGPV
 MLDEVRCCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCPTLTDGVIRLAGGKGSHEGR
 LEVYYRGQWGTVCDDGWTELNTYVVCRLGLGFKYQKQASANHFEESTGPIWLDDVSCS
 GKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGR
 VEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARTMAYFGEGKGPIHVDNVKCT
 GNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGNSNKESSLSSVCGLRLLHRRQ
 KRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTR
 SYAVRVGDYHTLVPEEFEEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSH
 VLPACLPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAPLLPKRFCEERYKGRFT
 GRMLCAGNLHEHKRVDSCQGDSSGGLMCERPGEWVVYGVTSWGYGCGVKDSPGV
 YTKVSAFVPWIKSVTKL

SEQ ID No: 20 (PLD3)

LAVVGFGALMTQLFLWEYGDLHLFGPNQRPAPCYDPCEAVLVESIPEGLDFPNASTGN
 PSTSQAWLGLLAGAHSSLDIASFYWTLTNDTHTQEPSAQQGEEVLRQLQTLAPKGVN
 VRIAVSKPSGPQPQADLQALLQSGAQVRMVDQMQLTHGVLHTKFWVVDQTHFYLGSA
 NMDWRSLTQVKELGVVMYNCCLARDLTKIFEAYWFLGQAGSSIPSTWPRFYDTRYNQ
 ETPMEICLNGTPALAYLASAPPLCPSGRTPDLKALLNVVDNARSFIYVAVMNYLPTLEF
 SHPHRFWPAIDDGLRRATYERGVKVRLLISCWGHSEPSMRAFLLSLAALRDNHTHSDIQ
 VKLFVVPADAEARIPYARVNHNKYMVTERATYIGTSNWSGNYFTETAGTSLLVTQNGR
 GGLRSQLEAIFLRDWDSPYSHDLDTADSVDGNACRL

SEQ ID No: 21 (RetSDR2)

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKLV
 LWDINKHGLEETAACKKGLGAKVHTFVVDCCSNREDIYSSAKKVKAIGDVSILVNNAGVV
 YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLA
 YCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVN
 RLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKQAQ

SEQ ID No:22 (APLP2)

MAATGTAAAAATGRLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAMFCGKLN
MHVNIQTGKWEPDPTGTKSCFETKEEVLQYCQEMYPELQITNVMEANQRVSIDNWCR
RDKKQCKSRFVTPFKCLVGEFVSDVLLVPEKQCQFFHKERMEVCENHQHWHTVVKEAC
LTQGMTLYSYGMLLPCGVDQFHGTEYVCCPQTKIIGSVSKEEEEEDEEEEEDEEED
YDVYKSEFPTEADLEDFTAAVDEDEDEDEEGEEVVEDRDYYYDTFKGDDYNEENPTE
PGSDGTMSDKEITHDVKAVCSQEAMTGPCRAVMWRWYFDLSKGKCVRFYGGCGGNR
NNFESEDYCMVCKAMIPPTPLPTNDVDVYFETSADDNEHARFQKAKEQLEIRHRNRM
DRVKKEWEEAELQAKNLPKAERQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAM
LNDRRRMALENYLAALQSDPPRPHRILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKA
AQMKSQVMTHLHVIEERRNQSLSLLYKVPYVAQEIQEEIDELLQEQRADMDQFTASISSET
PVDVRVSSEEESEEIPPFHPFHPFALPENEDTQPELYHPMKKGSGVGEQDGGGLIGAE
KVINSKNKVDENMVIDETLDVKEMIFNAERVGGLEEEERESVGPLREDFSLSSSALIGLLVI
AVAIATVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENPTYKYLEQM
QI

SEQ ID No:23 (APP)

MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPS
GTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR
CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPC
GIDKFRGVEFVCCPLAEESDNVDSADAEEDSDVWWGGADTDYADGSEDKVVEVAEE
EEVAEVEEEEEADDEDDEDGDEVEEEAEEPYEEATERTTSIATTTTTTTESVEEVVREV
CSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMVCGSAMS
QSLKTTQEPLARDPVKLPPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRE
MSQVMREWEEAERQAKNLPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVE
AMLNDRRRLALENYITALQAVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDP
KKAQIRSQVMTHLRVIYERMNQSLSLLYNVPVAEEIQDEVDELLQKEQNYSDDVLAN
MISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHSFGADSVANTENEVE
PVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLFFAEDVGS
NKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGY
ENPTYKFFEQMQN

SEQ ID No: 24 (SXN1)

MSGELPPNINIKEPRWDQSTFIGRANHFFTVDPRNILLTNEQLESARKIVHDYRQGIVPP
GLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTITGCMMTFYRTTPAVLFW
QWINQSFNAVVNYTNRSGDAPLTVNELGTAYVSATTGAVATALGLNALTGHVVSPLIGRF
VPFAAVAAANCINIPLMRQRELKVGIPVTDENGNRNLGESANAQAITQVVVSRILMAAP
GMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFATPLCCALFPQKSSMSVTSLE
AELQAKIQESHPELRRVYFNKGL

SEQ ID No: 25 (SORL1)

MATRSSRRESRLPFLFTLVALLPPGALCEVWTQRLHGGSAPLPQDRGFLVVQGDPREL
RLWARGDARGASRADEKPLRRKRSAALQPEPIKVYQVSLNDSHNQMVVHWAGEKS
NVIVALARDSLALARPKSSDVYVSYDYGKSFKKISDKLNFGLGNRSEAVIAQFYHSPADN
KRYIFADAYAQYLWITFDFCNTLQGFSSIPFRAADLLLHASKASNLLGLFDRSHPNKQLWKS
DDFGQTWIMIQEHVKSFSWGIDPYDKPNTIYIERHEPSGYSTVFRSTDFQSSRENQEVL
EEVRDFQLRDKYMFATKVVHLLGSEQQSSVQLWVSFGRKPMRAAQFVTRHPINEYYIA
DASEDQVFVVCVSHSNRNTNLYISEAEGLKFSLSLENVLYYSPGGAGSDTLVRYFANEPP
ADFHRVEGLQGVIATLINGSMNEENMRSVITFDKGGTWEFLQAPAFRTGYGEKINCELS
QGCSLHLAQRLSQLLNLQLRRMPILSKESAPGLIATGSVGKNLASKTNVYISSSAGARW
REALPGPHYTYWGDHGGIITAIAAQGMETNELKYSTNEGETWKTFFIFSEKPVFVYGLLTP
GEKSTVFTIFGSNKENVHSLILQVNATDALGVPCTENDYKLWSPSDERGNECLLGHKT
VFKRRTPHATCFNGEDFDRPVVVSNCSCSTREDYECDFGFKMSEDLSEVCVPDPEFSG
KSYSPPVPCPVGSTYRRTRGYRKISGDTCSGGDVEARLEGELVPCPLAEENEFILYAVR
KSIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQRLCLNGSTGQEVI
INSGLETVEALAFEPLSQLLYWVDAGFKKIEVANPDGDFRLTIVNSSVLDRPRALVLVPQ
EGVMFWTDWGDLPKGIYRSNMDGSAAYHLVSEDVKWPNGISVDDQWIYWTDAYLECI
ERITFSGQQRSVILDNLPHYPYAIKNEIYWDWSQLSIFRASKYSGSQMEILANQLTG
LMDMKIFYKGKNTGSNACVPRPCSLCLPKANNRSRSCRPEDVSSSVLPDGLMCDP
QGYQLKNNTCVKEENTCLRNQYRCSNGNCINSIWWCDFDNDGDMSDERNCPPTICD
LDTQFRCQESGTCIPLSYKCDLEDDCGDNDSESHCEMHQCRSDEYNCSSGMCIRSSW
VCDGDNDCRDWSDEANCTAIYHTCEASNFQCRNGHCIPQRWACDGDTCQDGSDED
PVNCEKKCNGFRCPNGTCIPSSKHCDGLRDCSDGSDEQHCEPLCTHFMDFVCKNRQQ
CLFHSMVCDGIIQCRDGSDEDAAFAGCSQDPEFHKVCDEFQFQCNQVCISLIWKCDG
MDDCGDYSDEANCENPTEAPNCSRYFQFRCENGHCIPNRWKCDRENDCGDWSDEKD
CGDSHILPFSTPGPSTCLPNYYRCSSGTCVMDTWVCDGYRDCADGSDEEACPLLANV
TAASTPTQLGRCDRFEFECHQPKTCIPNWKRCQDGHQDCQDGRDEANCPHSTLTCMS

REFQCEDGEACIVLSERCDCGFLDCSDESDEKACSDELTVYKVQNLQWTADFSGDVTLT
 WMRPKKMPSASCVYNVYYRVVGESIWKLETHSNKTNTVLKVLKPDTTYQVKVQVQCL
 SKAHNTNDFVTLRTPEGLPDAPRNLQLSLPREAEGVIVGHWAPPIHHTGLIREYIVEYSR
 SGSKMWASQRAASNFTIKNLLVNTLYTVRVAAVTSRGIGNWSDSKSITTIGKVI PPPDI
 HIDSYGENYLSFTLTMESDIKVNGYVVNLFWAFDTHKQERRTLNFRGSILSHKVGNLTA
 HTSYEISAWAKTDLGDSPLAFEHVMTRGVRPPAPSLKAKAINQTAVECTWTGPRNVVY
 GIFYATSFLDLYRNPKSLTTSLHNKTVIVSKDEQYLFLVRVVVPYQGPSSDYVVVKMIPD
 SRLPPRHLHVHTGKTSVVIKWESPYDSPDQDLLYAIKVDLIRKTD RSYKVKS RNSTVE
 YTLNKLEPGGKYHIIVQLGNMSKDSSIKITTVSLSAPDALKIITENDHVLLFWKSLALKEKH
 FNESRGYEIHMFD SAMNITAYLGNTTDNFFKISNLKMGHNYTFTVQARCLFGNQICGEP
 AILLYDELGSGADASATQAARSTDVA AVVVPILFLILLSLGVGFAILYTKHRRQLQSSFTAFA
 NSHYSSRLGSAIFSSGDDLGEDDEDAPMITGFSDDVPMVIA

SEQ ID No: 26 (SPC18)

MLSDFLDVRRMNRQLYYQVLNFGMIVSSALMIWKGLMVITGSESPIVVVLSGSMEP
 AFHRGDLLFLTNRVEDPIRVGEIVVFRIEGREIPVHRVLKIHEKQNGHIKFLTKGDNNAVD
 DRGLYKQGQHWLEKKDVVGRARGFVPYIGIVTILMNDYPKFYAVLFLGLFVLVHRE

SEQ ID No: 27 (SPC22)

MNTVLSRANSLFAFSLSVMAALTFGCFITTA FKDRSVPVRLHVSRI MLKNVEDFTGPRER
 SDLGFITSDITADLENIFDWNVKQLFLYLSAEYSTKNNALNQVVLWDKIVLRGDNPKLLLK
 DMKTKYFFFDDGNGLKGNRNVTLT LSWNVVPNAGILPLVTGSGHVSVPFPD TYEITKSY

SEQ ID No: 28 (SPC25)

MAAAAVQGGRRSGGSGGCSGAGGASNCGTGSGRSGLLDKWKIDDKPKIDKWDGSAV
 KNSLDDSAKKVLEKYKYVENFGLIDGRLTICTISCF FAIVALIWDYMHFPFESKPV LALCV
 ISYPLFMLS FVMMGILTIYTSYKEKSIFLVAHRKDPTGMDPDDIWQLSSSLKRFDDKYTLK
 LTFISGR TKQQREAEFTKSI AKFFDHSGTLVMDAYEPEISRLHDSLAIERKIK

SEQ ID No: 29 (stearoyl-CoA desaturase)

MPAHL LQDDISSSYTTTTTITAPPSRVLQNGGDKLETMPLYLEDDIRPDIKDDIYDPTYKD
 KEGPSPKVEYVWRNIILMSLLHLGALYGITLIPTCKFYTWLWGVFYFVSALGITAGAHRL
 WSHRSYKARLPLRLFLIIANTMAFQNDVYEW ARDHRAHHKFSETHADPHNSRRGFFFS
 HVGWLLVRKHPAVKEKGSTLDLSDEAEKLV MFQRRYYKPGLLMMCFILPTLV PWYFW

GETFQNSV FVATFLRYAVVLNATWLVNSAAHLFGYR PYDKNISPRENILVSLGAVGEGF
 HNYHHSFPYDYSASEYRWHINFTTFFIDCMAALGLAYDRKKVSKAAILARIKRTGDGNYK
 SG

SEQ ID No: 30 (TMP21)

MSGLSGPPARRGPFPLALLLLFLLGPRLVL AISFHLPINSRKCLREEIHKDLLVTGAYEISD
 QSGGAGGLRSHLKITDSAGHILYSKEDATKGKFAFTTEDYDMFEVCFESKGTGRIPDQL
 VILDMKHGVEAKNYEEIAKVEKLPLEVELRRLEDLSESIVNDFAYMKKREEEMRDTNES
 TNTRVLYFSIFSMFCLIGLATWQVFYLRFFFKAKKLIE

SEQ ID No: 31 (VLCAD)

MSGCGLFLRTTAAARACRGLVVSTANRRLLRTSPPVRAFAKELFLGKIKKKEVFPFPEV
 SQDELNEINQFLGPVEKFFTEEVD SRKIDQEGKIPDETLEKLKSLGLFGLQVPEEYGGGLG
 FSNTMYSRLGEIISMDGSITVTLAAHQAIGLKG ILAGTTEEQKAKYLPKLASGEHIAAFCLT
 EPASGSDAASIRSRATLSEDKKH YILNGSKVWITNGGLANIFTVFAKTEVVDS DGSVKDK
 ITAFIVERDFGGVTNGKPEDKLGIRG SNTCEVHFENTKIPVENILGEVGDGFKVAMNINLS
 GRFSMGSVVAGLLKR LIEMTA EYACTRKQFNKRLSEFGLIQEKFALMAQKAYVMESMTY
 LTAGMLDQPGFPDCSIEAAMVKVFSSEA AWQCVSEVLQILGGLGYTRDYPYERILRDTR
 ILLIFEGTNEILRMYIALTGLQHAGRI LTTRIHELKQAKVSTVMDTVGRRLRDSLGR TVDLG
 LTGNHGVVHPSLADSANKFEENTYCFGR TVETLLLRFGKTIMEEQVLVKRVANILINLYG
 MTAVLSRASRSIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKYAPENLDEQIKKVS
 QQILEKRAYICAHPLDRTC

SEQ ID No: 32 (YME1L1)

MFSLSSTVQPQVTVPLSHLINA FHTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSEPSL
 NLRDLGLSELKIGQIDQLVENLLPGFCKGKNIS SHWHTSHVSAQSFFENKYGNLDIFSTL
 RSSCLYRHHSRALQSICSDLQYWPVFIQSRGFKTLKSRT RRLQSTSERLAETQNIAPSF
 VKGFLLRDRGSDVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDSLRRTR
 LILFVLLLFGIYGLLKNPFLSVRFRTTTGLDS AVDPVQMKNVTFEHVKGV EEAQELQEV
 VEFLKNPQKFTILGGKLPKGILLVGPPGTGKTLLARAVAGEADV PFYYASGSEFDEM FV
 GVGASRIRNLFREAKANAPCVIFIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPN
 EGVIIIGATNFPEALDNALIRPGRFDMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDP EIIA
 RGTVGFGSGAELENLVNQAALKA AVDGKEMVTMKELEFSKDKILMGPERRSVEIDNKNKT
 ITAYHESGHAI IAYYTKDAMPINKATIMPRGPTLGHV SLLPENDRWNETRAQLLAQMDVS

MGGRVAEELIFGTDHITTGASSDFDNATKIAKRMVTKFGMSEKLGVM TYSDTGKLS PET
QSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEALLTYETLDAKEIQIVLEGKKLEVR

SEQ ID No: 33 (LAPTM4B)

MVNYAWAGRSQRKLWWSVAVLTCKSVVRPGYRGGLQARRSTLLKTCARARATAPG
AMKMPVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSE
LGGDFEFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAIT
VLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYLISCVWNCYRYING
RNSSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA

SEQ ID No: 34 (S100alpha)

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKD VDAVDKVM
KELDENG DGEVDFQEYVVLVAALT VACNNFFWENS

SEQ ID No:35 (Cadherin EGF LAG seven-pass G-tpe receptor 2)

MRSPATGVPLPTPPPLLLLLLLLLLPPPLLGDQVGPCRSLSRGRGSSGACAPMGWLC
PSSASN LWLYTSRCRDAGTELTGHLVPHHDGLRWWCPESEAHIPPAPEGCPWSCRL
LGIGGHLSPQGKLTLP EEHPCLKAPRLRCQSCKLAQAPGLRAGERSPEESLGGRKRN
VNTAPQFQPPSYQATVPENQPAGTPVASLRAIDPDEGEAGRLEYTMDALFDSRSNQFF
SLDPVTGAVTTAEELDRETKSTHVFRVTAQDHGMPRRSALATLTILVTDTNDHDPVFEQ
QEYKESLRENLEVG YEVLTVRATDGDAPPNANILYRLL EGSGGSPSEVFEIDPRSGVIRT
RGPVDREEVESYQLTVEASDQGRDPGPRSTTAAVFLSVEDDNDNAPQFSEKRYVVQV
REDVTPGAPVLRVTASDRDKGSNAV VHYSIMSGNARGQFYLDAQTGALDVVSPLDYET
TKEYTLRVRAQDGGRPPLSNVSGLVTVQVLDINDNAPIFVSTPFQATVLESVPLGYLV LH
VQAIDADAGDNARLEYRLAGVGHDFPFTINNGTGWISVAAELDREEVDFYSFGVEARDH
GTPALTASASVSVTVLDVNDNNPTFTQPEYTVRLNEDAAVGTSVTVSAVDRDAHSVIT
YQITSGNTRNRFSITSQSGGGLVSLALPLDYKLERQYVLAVTASDGTRQDTAQIVNVTD
ANTHRPVFQSSH YTVNVNEDRPAGTTVVLISATDEDTGENARITYFMEDSIPQFRIDADT
GAVTTQAELDYEDQVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSYQGS
VYEDVPPFTSVLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRTLRRLDRE
NVAQYVLRAYAVDKGMPPPARTPMEVTVTVLDVNDNPPVFEQDEFDVFVEENSPIGLAV
ARVTATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDLDYEDRPEYVLVIQATSA
PLVSRATVHVRLDRNDNPPVLGNFEILFN NYVTNRSSSFPGGAIGRVPAHDPDISDSLT
YSFERGNELSLVLLNASTGELKLSRALDNNRPLEAIMSVLVSDGVH SVTAQCALRVTIITD

EMLTHSITLRLEDMSPERFLSPLLGLFIQAVAATLATPPDHVVVFNVQRD TDAPGGHILN
 VLSVVGQPPGPGGGPPFLPSED LQERLYLNRSLLTAISAQRVLPFDDNICLREPCENYM
 RCVSVLRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGFTGDYCETEVDLCYSRPCGPH
 GRCRSREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCKNGGTCVNLLVGGFKDCDP
 SGDFEKPYPYCQVTTRSFP AHSFITFRGLRQRFHFTLALS FATKERDGLLLYNGRFNEKHD
 FVALEVIQEQVQLTFSAGESTTTVSPFVPGGVSDGQWHTVQLKYYNKPLL GQTGLPQG
 PSEQKVAVVTVDGCDTGVALRFGSVLGNYSCAAQGTQGGSKKSLDLTG PLLLGGVPDL
 PESFPVRMRQFVGCMRN LQVDSRHIDMADFIANNGTVPGCPAKKNVCDSNTCHNGGT
 CVNQWDAFSCCEPLGFGGKSCAQEMANPQHFLGSSLVAWHGLSLPISQPWYLSLMFR
 TRQADGVLLQAITRGRSTITLQLREGHVMLSVEGTGLQASSLRLEPGRANDGDWHHAQ
 LALGASGGPGHAILSFDY GQQRAEGNLGPRLHGLHLSNITVGGIPGPAGGVARGFRGC
 LQGVVRVSDTPEGVNSLDPSHGESINVEQGCSLPDPCDSNPCPANSYCSNDWDSYSCS
 CDPGYYGDNCTNVCDLNPCEHQSVCTRKPSAPHGYTCECPPNYLGPYCETRIDQPCP
 RGWWGHPTCGPCNCDVSKGFDPCDNKTSGECHCKENHYRPPGSPTCLLCDCYPTGS
 LSRVCDPEDGQCPCPKPGVIGRQCDCRCDNPFAEVT TNGCEVNYDSCPRAIEAGIWWPR
 TRFGLPAAAPCPKGSFGTAVRHCD EHRGWLPNLFNCT SITFSELKGFAERLQRNESG
 LDSGRSQQLALLLRNATQHTAGYFGSDVKVAYQLATRLLAHESTQRGFGLSATQDVHF
 TENLLRVGSALLDTANKRHWELIQQT EGGTAWLLQH YEAYASALAQNMRHTYLSPTIV
 TPNIVISVVRLDKGNFAGAKLP RYEALRGEQPPDLETTVILPESVFRET PPVVRPAGPGE
 AQEPEELARRQRRHPELS QGEAVASVIIYRTL AGLLPHNYDPDKRSLRVPKRPIINTPVV
 SISVHDDEELLPRALDKPVT VQFRLLETEERTK PICVFWNHSILVSGTGGWSARGCEVV
 FRNESHVSCQCNHMTSFAVLMDVSRREN GEILPLKTLTYVALGVT LAALLTFFFLTLLRI
 LRSNQHGIRRNLTAA LGLAQLVFL LGINQADLPFACTVIAILLHFLYLCTFSWALLEALHLY
 RALTEVRDVNTGPMRFY YMLGWGVPAFITGLAVGLDPEGYGNPDFCWLSIYDTLIWSF
 AGPVAFAVSMSVFLYILAARASCAAQRQGF EKKGPVSGLQPSFAVLLLLSATWLLALLS
 VNSDTLLFH YLFATCNCIQGPFI FLSYVVL SKEVRKALKLACSRKPSPDPALTTKSTLTSS
 YNCPSPYADGRLYQPYGDSAGSLHSTSRSGKSQPSYIPFLLREESALNPGQGPPGLGD
 PGS LFEGQDQQHDPD TDSDSLSEDDQSGSYASTHSSDSEEEEEEEEEEEA AFPGE
 QGWDSLLGPGAERLPLHSTPKDGGPGPGKAPWPGDFGTTAKESSGNGAPEERLREN
 GDALSREGSLGPLPGSSAQPHKGILKKKCLPTISEKSSLLRLPLEQCTGSSRGSSASEG
 SRGGPPPRPPPRQSLQEQLNGVMPIAMSIKAGTVDEDSSGSEFLFFNFLH

SEQ ID No:36 (Calsyntenin)

MLRRPAPALAPAARLLLGLLGGGWWAARVNHKHPWLEPTYHGIVTENDNTVLLDPP
 LIALDKDAPLRFASFVTVTKEGEICGFKIHGQNVPFDAVVVDKSTGEGVIRSEKLDLDC
 ELQKDYSFTIQAYDCGKGPDGTNVKKSHKATVHIQVNDVNEYAPVFKEKSYKATVIEGK
 QYDSILRVEAVDADCSPQFSQICSYEIITPDVPFTVDKDGVIKNTTEKLNKGKEHQYKLTVT
 AYDCGKKRATEDVLVKISIKPTCTPGWQGWNNRIEYEPGTGALAVFPNIHLETCDPVA
 SVQATVELETSHIGKGCDDRTYSEKSLHRLCGAAAGTAELLPSPSGSLNWTMGLPTDN
 GHDSQVFEFNGTQAVRIPDGVVSVSPKEPFTISVWMRHGPFGRKKETILCSDKTDN
 NRHHYSLYVHGCRLIFLFRQDPSEEKKYRPAEFHWKLNQVCDEEWHHYVLNVEFPSVT
 LYVDGTSHEPFSVTEDYPLHPSKIETQLVVGACWQEFSGVENDNETEPVTVASAGGDL
 HMTQFFRGNLAGLTLRSGKLADKKVIDCLYTCKEGLDLQVLEDSGRGVQIQAHPSQLVL
 TLEGEDLGELDKAMQHISYLNRSRQFPPTGIRRLKITSTIKCFNEATCISVPPVDGYVMVLQ
 PEEPKISLSGVHHFARAASEFESSEGVFLFPELRIISTITREVEPEGDGAEDPTVQESLVS
 EEIVHDLDTCEVTVEGEELNHEQESLEVDMARLQQKGIEVSSSELGMTFTGVDTMASYE
 EVLHLLRYRNWHARSLDRKFKLICSELNGRYISNEFKVEVNVIIHTANPMEHANHMAAQ
 PQFVHPEHRSFVDLSGHNLANPHFPAVVPSTATVVIVVCVSFLVFMILGVFRIRAAHRRRT
 MRDQDTGKENEMDWDDSAITITVNPMEYEDQHSSEEEEEEEEEEEEESEEDGEEDDITS
 AESESSEEEEGEQGDPQNAIRQQQLEWDDSTLSY

SEQ ID No: 37 (visinin-like 1)

MGKQNSKLAPEVMEDLVKSTEFNEHELKQWYKGFLKDCPSGRLNLEEFQQLYVKFFPY
 GDASKFAQHAFRTFDKNGDGTIDFREFICALSITSRGSFEQKLNWAFNMYDLGDGKIT
 RVEMLEIEAIYKMVGTVIMMKMNEDGLTPEQRVDKIFSKMDKNKDDQITLDEFKEAAKS
 DPSIVLLLQCDIQK

SEQ ID No: 38 (BACE1)

MAQALPWLLLWMGAGVLPAGHTQHGIPLRSLGGLGAPLGLRLPRETDEEPEEPGRR
 GSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNVLDTGSSNFAVGAAPHPFLHRYQ
 RQLSSTYRDLRKGVYVPYTQGWEGELGTDLLCGAGFPLNQSEVLASVGGSMIIGGID
 HSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPLPKV
 FEA AVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRTI
 LPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSAC
 HVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQ
 WRCLRCLRQQHDDFADDISLLK

SEQ ID No: 39 (CELSR2)

MRSPATGVPLPTPPPLLLLLLLLLLPPPLLDQVGPCRSLGSRGRGSSGACAPMGWLC
PSSASNLWLYTSRCRDAGTELTGHLVPHHDGLRVWCPESHAHIPLPPAPEGCPWSCRL
LGIGGHLSPQGKLTLP EEHPCLKAPRLRCQSCKLAQAPGLRAGERSPEESLGGRKRNRN
VNTAPQFQPPSYQATVPENQPAGTPVASLRAIDPDEGEAGRLEYTMDALFDSRSNQFF
SLDPVTGAVTTAEELDRETKSTHVFRVTAQDHGMPRRSALATLTILVTDNDHDPVFEQ
QEYKESLRENLEVG YEVLTVRATDGDAPPNANILYRLLEGSGGSPSEVFEIDPRSGVIRT
RGPVDREEVESYQLTVEASDQGRDPGPRSTTA AVFLSVEDDNDNAPQFSEKRYVVQV
REDVTPGAPVLRVTASDRDKGSNAV VHYSIMSGNARGQFYLDAQTGALDVVSPLDYET
TKEYTLRVRAQDGGRPPLSNVSGLVTVQVLDINDNAPIFVSTPFQATVLESVPLGYLV LH
VQAIDADAGDNARLEYRLAGVGHDFPFTINNGTGWISVAAELDREEVDFYSFGVEARDH
GTPALTASASVSVTVLDVNDNNPTFTQPEYTVRLNEDAAVGTSVTVSAVDRDAHSVIT
YQITSGNTRNRFSITSQSGGGLVSLALPLDYKLERQYVLAVTASDGTRQDTAQIVNVNTD
ANTHRPVFQSSHYTVNVNEDRPAGTTVLISATDEDTGENARITYFMEDSIPQFRIDADT
GAVTTQAELDYEDQVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSYQGS
VYEDVPPFTSVLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRTLRRLDRE
NVAQYVLRAYAVDKGMPPARTPMEVTVTVLDVNDNPPVFEQDEFDVFEENSPIGLAV
ARVTATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDLDYEDRPEYVLVIQATSA
PLVSRATVHVRLLDRNDNPPVLGNFEILFN NYVTNRSSSFPGGAIGRVPAHDPDISDSL T
YSFERGNELSLVLLNASTGELKLSRALDNNRPLEAIMSVLVSDGVH SVTAQCALRVTIITD
EMLTHSITLRLEDMSPERFLSPLLGLFIQAVAATLATPPDHVVVFNVQRD TDAPGGHILN
VSLSVGQPPPGPGGGGPPFLPSED LQERLYLNRSLT AISAQRVLPFDDNICLREPCENYM
RCVSVLRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGFTGDY CETEVDLCYSRPCGPH
GRCRSREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCKNGGTCVNLLVGGFKDCDP
SGDFEKPYPYCQVTTRSFP AHSFITFRGLRQRFHFTLALS FATKERDGLLLYNGRFNEKHD
FVALEVIQEQQVQLTFSAGESTTTVSPFVPGGVSDGQWHTVQLKYYNKPLL GQTGLPQG
PSEQKVAVVTVDGCDTGVALRFGSVLGNYSCAAQGTQGGSKKSLDLTG PLLLGGVPDL
PESFPVRMRQFVGCMRNLQVDSRHIDMADFIANN GTVPGCPAKKNVCDSNTCHNGGT
CVNQWDAFSCECPLGFGGKSCAQEMANPQHFLGSSLVAWHGLSLPISQPWYLSLMFR
TRQADGVLLQAITRGRSTITLQLREGHVMLSVEGTGLQASSLRLEPGRANDGDWHHAQ
LALGASGGPGHAILSFDY GQQRAEGNLGPRLHGLHLSNITVGGIPGPAGGVARGFRGC
LQGV RVSDTPEGVNSLDPSHGESINVEQGCSLPDPCDSNPCPANSYCSNDWDSYSCS
CDPGYYGDNCTNVCDLNPCEHQSVCTRKPSAPHGYTCECPPNYLGPYCETRIDQPCP
RGWWGHPTCGPCNCDVSKGFDPDCNKTSGECHCKENHYRPPGSPTCLLCDCYPTGS

LSRVCDPEDGQCPCCKPGVIGRQCDCRCDNPFAEVTTNNGCEVNYDSCPRAIEAGIWWPR
 TRFGLPAAAPCPKGSFGTAVRHCDHRGWLPNLFNCTSITFSELKGFAERLQRNESG
 LDSGRSQQLALLRNATQHTAGYFGSDVKVAYQLATRLLAHESTQRGFGLSATQDVHF
 TENLLRVGSALLDTANKRHWELIQQTEGGTAWLLQHYEAYASALAQNMRYHTYLSPTIV
 TPNIVISVVRDLKGNFAGAKLPRYEALRGEQPPDLETTVILPESVFRETTPVVRPAGPGE
 AQEPEELARRQRRHPELSQGEAVASVIIYRTLGLLPHNYDPDKRSLRVPKRPIINTPVV
 SISVHDDEELLPRALDKPVTQFRLLTEERTKPICVFWNHSILVSGTGGWSARGCEVV
 FRNESHVSCQCNHMTSFAVLMDVSRRENGEILPLKTLTYVALGVTLAALLLTFFFLTLLRI
 LRSNQHGIRRNLTAAALGLAQLVFLGGINQADLPFACTVIAILLHFLYLCTFSWALLEALHLY
 RALTEVRDVNTGPMRFYYMLGWGVPAFITGLAVGLDPEGYGNPDFCWLSIYDTLIWSF
 AGPVAFVSMVFLYILAAARASCAAQRQGFEEKKGPVSGLQPSFAVLLLLSATWLLALLS
 VNSDTLLFHLYFATCNCIQGPFIFLSYVVLKSKEVRKALKLACSRKPSPDPALTTKSTLTSS
 YNCPSPYADGRLYQPYGDSAGSLHSTSRSGKSQPSYIPFLLREESALNPGQGPPGLGD
 PGSIFLEGQDQHDPTDSDSDLSLEDDQSGSYASTHSSDSEEEEEEEEEEEAAFPGE
 QGWDSLLGPGAERLPLHSTPKDGGPGPGKAPWPGDFGTAKESSGNGAPEERLREN
 GDALSREGSLGPLPGSSAQPHKGILKKKCLPTISEKSSLLRPLEQCTGSSRGSSASEG
 SRGGPPPRPPPRQSLQEQLNGVMPIAMSIKAGTVDEDSSGSEFLFFNFLH

SEQ ID No: 40 (FADS2)

MGKGGNQGEAAEREVSVPFTSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQ
 RVIGHYAGEDATDAFRAFHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALR
 KTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL
 QHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNM
 LHVFLGEWQPIEYGGKKLKYLPYNHQHEYFFLIGPPLLIPMYFYQYQIIMTMIVHKNWVDL
 AWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQMNHIVMEIDQEAYRDWFS
 SQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQE
 KPLLRAALLDIIRSLKKSGKLWLDAYLHK

SEQ ID No: 41 (NogoA)

MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERT
 EFSELEYSEMGSFSVSPKAESAVIVANPREEIVKNKDEEEKLVSNILHNQQELPTALT
 KLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAA
 GGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPF
 NPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETD

YVTTDNLT KVTEEVVANMPEGLTPDLVQEACESELNEVTG TKIAYETKMDLVQTSEVMQ
 ESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYE
 SIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAE
 PAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDD SIPDVPQKQDETVM LVK
 ESLTETS FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIP
 LQMEELSTAVYSNDDLFISKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDL
 EVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LLLP
 PDVSALATQAEIESIVKPKVLVKEAEKKLP SDTEKEDRSPSAIFSAELSKTSVVDLLYWRD
 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL
 ESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNG
 LTL LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE

SEQ ID No: 42 (OS-9)

MAAETLLSLLGLLLLGLLLPASLTGGVGSLNLEELSEMRYGIEILPLPVMGGQSQSSDV
 VIVSSKYKQRYECRLPAGAIHFQREREEETPAYQGPGIPELLSPMRDAPCLLKT KDWWT
 YFCYGRHIQQYHMEDSEIKGEVLYLGYYQSAFDWDD ETAKASKQHRLKRYHSQTYG
 NGSKCDLNGRPREAEVRFLCDEGAGISGDYIDRVDEPLSCSYVLTIRTPRLCPHPLLRP
 PPSAAPQAILCHPSLQPEEY MAYVQRQAVDSKQYGD KIIIEELQDLGPQVWSETKSGVA
 PQKMAGASPTKDDSKDSDFWKMLNEPEDQAPGGEEVPAEEQDPSPEAADSASGAPN
 DFQNNVQVKVIRSPADLIRFIEELKGGTKKGKPNIGQE QPVDDAAEVPQREPEKERGDP
 ERQREMEEEDEDEDEDEDEDEDERQLLGEFEKELEGILLPSDRDRLRSEVKAGMERELE
 NIIQEASPALPPTKEKELDPDGLKKESERDRAMLALTSTLNKLIKRL EEKQSPELVKKHKKK
 RVVPKKPPSPQPT EEDPEHRVRVRVTKLRLGGPNQDLTVLEMKREN PQLKQIEGLVK
 ELLEREGLTAAGKIEIKIVRPWAEGTEEGARWLTDEDTRNLKEIFFNILVPGAEEAQKER
 QRQKELESNYRRVWGSPGGEGTGDLDEFDF

SEQ ID No: 43 (PDGFRB)

MRLPGAMPALALKGELLLL SLLLLLEPQISQGLVVTPPGPELV LNVSSTFVLTCSGSAPV
 VWERMSQEPPQEMAKAQDGT FSSVLTLTNLTGLDTGEYFCTHND SRGLETDERKRLYI
 FVPDPTVGFLPNDAEELFIFLTEITEITIPCRVTD PQLVVTLHEKKGDVALPVYDHQRGF
 SGIFEDRSYICKTTIGDREVDSDAYYVYRLQVSSINVS VNAVQTVVRQGENITLMCIVIGN
 EVVNF EW TYPRKEVIGRLVEPVTD FLLDMPYHIRSILHIPS AELEDSGTYTCNVTESVND
 HQDEKAINITVVESGYVRLLGEVGT LQFAELHRSRTLQVVF EAYPPPTVLWFKDNRTL G
 DSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAF HEDA EVQLSFQLQINVPV

RVLELSESHPDSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEEEESQ
 LETNVTYWEEEEEQEFVVSTLRLQHVDRLPSVRCTLRNAVGGDTQEIVVPHSLPFKVVV
 ISAILALVVLTIISLIILMLWQKKPRYEIRWKVIESVSSDGHYIYVDPMQLPYDSTWELPR
 DQLVLGRTLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIM
 SHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAEL
 YSNALPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYM
 APYDNYVPSAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAAR
 NVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGI
 LLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPF
 SQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYT
 AVQPNEGDNDYIIPDPKPPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEP
 EPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL

SEQ ID No: 44 (PTK7)

MGAARGSPARPRRLPLLSVLLLPLGGTQTAIVFIKQPSSQDALQGRRALLRCEVEAPG
 PVHVYWLLDGAPVQDTERRFAQGSSLSFAAVDRLQDSGTFQCVARDDVTGEEARSAN
 ASFNIKWIEAGPVVLKHPASEAEIQPQTQVTLRCHIDGHPRPTYQWFRDGTPLSDGQSN
 HTVSSKERNLTLRPAGPEHSGLYSCCAHSAFGQACSSQNFTLSIADES FARVVLAPQDV
 VVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATVFANGSLLLTQVR
 PRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGSEERVTCCLPPKGLPEPS
 VWEHAGVRLPTHGRVYQKGHELVLANIAESDAGVYTCHAAANLAGQRRQDVNITVATV
 PSWLKKPQDSQLEEGKPGYLDCLTQATPKPTVWYRNQMLISED SRFEVFKNGTLRIN
 SVEVYDGTWYRCMSSTPAGSIEAQARVQVLEKLKFTPPPQPQQCMEFDKEATVPCSAT
 GREKPTIKWERADGSSSLPEWVTDNAGTLHFARVTRDDAGNYTCIASNGPQQGQIRAHVQ
 LTVAVFITFKVEPERTTVYQGHTALLQCEAQGDPKPLIQWKGKDRILDPTKLGPRMHIFQ
 NGSLVIHDVAPEDSGRYTCIAGNSCNIKHTEAPLYVVDKPVPEESEGGSPPPYKMIQTI
 GLSVGAAYAYIIAVLGLMFYCKKRCKAKRLQKQPEGEPEMECLNGGPLQNGQPSAEI
 QEEVALTSLGSGPAATNKRHSTSDKMHFPRSSLQPITTLGKSEFGEVFLAKAQGLEEGV
 AETLVLVKSLQSKDEQQQLDFRRELEMFGKLNHANVVRLLGLCREAEPHYMVLEYVDL
 GDLKQFLRISKSKDEKLKSQPLSTKQKVALCTQVALGMEHLSNNRFVHKDLAARNCLVS
 AQRQVKVSALGLSKDVYNSEYYHFRQAWVPLRWMSPEAILEGDFSTKSDVWAFGVLM
 WEVFTHGEMPHGGQADDEV LADLQAGKARLPQPEGCP SKLYRLMQRCWALSPKDRP
 SFSEIASALGDSTVDSKP

SEQ ID No: 45 (UGCGL1)

MGCKGDASGACAAGALPVTGVCYKMGVLVVLTVLWLFSSVKADSKAITTSLTTKWFST
PLLEASEFLAEDSQEKFWNFVEASQNIGSSDHDGTDYSYYHAILEAAFQFLSPLQQNL
FKFCLSLRSYSATIQAQQIAADEPPPEGCNSFFSVHGGKKTCESDTLEALLLTASERPKP
LLFKGDHRYPPSSNPESPVVIFYSEIGSEEFNSFHRQLISKSNAKGKINYVFRHYIFNPRKEP
VYLSGYGVELAIKSTEYKAKDDTQVKGTEVNTTVIGENDPIDEVQGFLFGKLRDLHPDLE
GQKELRKHLVESTNEMAPLKVWQLQDLSFQTAARILASPVELALVVMKDLSQNFPTKA
RAITKTAVSSELRTVEEENQKYFKGTLGLQPGDSALFINGLHMDLDTQDIFSLFDVLRNE
ARVMEGLHRLGIEGLSLHNVKLNIQPSEADYAVDIRSPAISWVNNLEVDSRYNSWPSS
LQELLRPTFPGVIRQIRKNLHNMVFIVDPAHETTAELMNTAEMFLSNHIPLRIGFIFVND
EDVDGMQDAGVAVLRAYNYVAQEVDDYHAFQTLTHIYNKVRTGEKVKVEHVSVLEKK
YPYVEVNSILGIDSAYDRNRKEARGYYEQTGVGPLPVVLFNGMPFEREQDPDELETIT
MHKILETTTTFFQRAVYLGELPHDQDVVEYIMNQPNVPRINSRILTAERDYDLTASN
FVDDYARFTILDSQGKTA AVANS MN YLTKKGMSSKEIYDDSFIRPVTFWIVGDFD
SPSG RQLLYDAIKHQKSSNNVRISMINNPAKEISYENTQISRAIWAALQTQTSNA
AKNFITKMAK EGAAEALAAGADIAEFSVGGMDFSLFKEVFESSKMDFILSHAVYCRD
VLKLLKKGQRAVIS NGRIIGPLEDSELFNQDDFHLLENIILKTSGQKIKSHIQQLR
VEEDVASDLVMKVDALLSA QPKGDPRIEYQFFEDRHSIAIKLRPKEGETYFDV
VAVVDPVTREAQRLAPLLLVL AQLINM NLRVFMNCQSKLSDMPLKSFYRYV
LEPEISFTSDNSFAKGPIAKFLDMPQSPLFTLNLT PESWMVESVRTPYDL
DNIYLEEVDSVVA AEYELEYLLLEGHCYDITTGQPPRGLQFTLG TSANPV
IVDTIVMANLGYFQLKANPGAWILRLRKGRSEDIYRIYSHDGTDSPPDADEV
VIV LNNFKSKIIVKVQKKADMVNEDLLSDGTSENE SGFWD SFKWGFTGQKTEE
VKQDKDD IINIFSVASGHLYERFLRIMMLSVLKNTKTPVKFWFLKNYLSPTF
KEFIPYMANEYNFQYE LVQYKWPRWLHQQTEKQRIIWGYKILFLDVLFP
LVVDKFLFVDADQIVRTDLKELRDFNL DGAPYGYTPFCDSRREMDGYR
FWKSGYWASHLAGRKYHISALYVVDLKKFRKIAAGD RLRGQYQGLS
QDPNSLSNLDQDLPNNMIHQVPIKSLPQEWLWCETWCDDASKKRAKTI
DLCNNPMTKEPKLEAAVRIVPEWQDYDQEIKQLQIRFQKEKETGALYKEK
TKEPSREGP QKREEL

SEQ ID No: 46 (CtnnB1)

MATQADLMELDMAMEPDRKAAVSHWQQQSYLDSGIHSGATTTAPSLSGKGNPEEEDV
DTSQVLYEWEQGFSSQFTQEQQVADIDGQYAMTRAQRVRAAMFPETLDEGMQIPSTQF
DAAHPTNVQRLAEP SQMLKHAVVNLINYQDDAELATRAIPELTKLLNDEDQVVVN
KAAV MVHQLSKKEASRHAIMRSPQMVSIVRTMQNTNDVETARCTAGTLHNL
SHHREGLLAIF

KSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNV
 KFLAITTDCQLILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSSVCSN
 KPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGLTLVQLLGS
 DDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHL
 TSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQ
 GAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIV
 IRGLNTIPLFVQLLYSPIENIQRVAAGVLCelaQDKEAAEAIEAEGATAPLTELLHSRNEGV
 ATYAAAVLFRMSEDKPQDYKKRLSVELTSSLFRTEPMAWNETADLGLDIGAQGEPLGY
 RQDDPSYRSFHSGGYGQDALGMDPMMHEMGGHHPGADYPVDGLPDLGHAQDLMD
 GLPPGDSNQLAWFDTDL

SEQ ID No: 47 (CtnnA1)

MTAVHAGNINFKWDPKSLEIRTLAVERLLEPLVTQVTTLVNTNSKGPSNKKRGRSKKAH
 VLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKAAAGEFADDPCSS
 VKRGNMVRAAPALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGNQY
 KALKPEVDKLNIMAAKRQQELKDVGHRDQMAAARGILQSNVPILYTASQACLOHPDVAA
 YKANRDLIYKQLQQAQVTGISNAAQATASDDASQHQQGGGGGELAYALNNFDKQIIVDPLS
 FSEERFRPSLEERLESIISGAALMADSSCTRDDRERIVAECNAVRQACRTCSEYMG
 AGRKERSDALNSAIDKMTKKTRDLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNE
 KEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVMSASQLEAGCPQVINAATWAL
 APKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITSIDDFLAVSENHILEDVNKCVIALQ
 EKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKVLEATKLLSNTVMPRFTEQ
 VEAAVEALSSDPAQPMDENEFIDASRLVYDGIRDIRKAVLMIRTPEELDDSDFETEDFDV
 RSETSVQTEDDQLIAGQSARAIMAQLPQEQAQKIREQVASFQEEKSKLDAEVSKWDDS
 GNDIIVLAKQMCMIMMEMTDFTRGKGPLKNTSDVISAACKIAEAGSRMDKLGRITRDHC
 PDSACKQDLLAYLQRIALYCHQLNICKVKAQVQNLGGELVVSGNCDTCGALQGLKGW
 PPPLCLATHWVDSAMSLIQAANKLMNAVVTQVKASYVASTKYQKSQGMASLNLPAVSM
 KMKAPEKKPLVKREKQDETQTKIKRASQKKHVNPVQALSEFKAMDSI

SEQ ID No: 48 (CtnnA2)

MTSATSPIILKWDPKSLEIRTLTVERLLEPLVTQVTTLVNTSNKGPSGKKKGRSKKAHVLA
 ASVEQATQNFLEKGEQIAKESQDLKEELVAAVEDVRKQGETMRIASSEFADDPCSSVKR
 GTMVRAARALLSAVTRLLILADMADVMRLLSHLKIVEEAEAVKNATNEQDLANRFKEFG
 KKMVKLNYVAARRQQELKDPHCRDEMAAARGALKKNATMLYTASQAFLRHPDVAATR

ANRDYVFKQVQEAIAGISNAAQATSPTDEAKGHTGIGELAAALNEFDNKIILDPMTFSEA
 RFRPSLEERLESIISGAALMADSSCTRDDRRERIVAECNAVRQALQDLLSEYMNNTGRK
 EKGDP LNIAIDKMTKKTRDLRRQLRKAVMDHISDSFLETNVPLLVLIEAAKSGNEKEVKE
 YAQVFREHANKLVEVANLACISISNNEEGVKLV RMAATQIDSLCPQVINAALT LAARPQSK
 VAQDNMDVFKDQWEKQVRVLTEAVDDITSVDDFLSVSENHILEDVNKCVIALQEGD VDT
 LDRTAGAIRGRAARVIHIINAEMENYEAGVYTEKVL EATKLLSETVMPRFAEQVEVAIEAL
 SANVPQPFEENE FIDASRLVYDGVDRDIRKAVLMIRTPEELEDDSDFEQEDYD VRRGTSV
 QTEDDQLIAGQSARAIMAQLPQEEKAKIAEQVEIFHQE KSKLDAEVAKWDDSGNDIIVLA
 KQMCMIMMEMTDFTRGKGPLKNTSDVINA AKKIAEAGSRMDKLARAVADQCPDSACKQ
 DLLAYLQRIALYCHQLNICKSVKAEVQNLGGELIVSGTGVQSTFTTFYEVD CDVIDGGRA
 SQLSTHLPTCAEGAPIGSGSSDSSMLDSATSLIQA AKNLMNAVVLTVKASYVASTKYQK
 VYGTA AVNSPVVSWKMKAPEKKPLVKREKPEEFQTRVRRGSQKKHISP VQALSEFKAM
 DSF

SEQ ID No: 49 (CtnnD1)

MDDSEVESTASILASVKEQEAQFEKLTRALEEERRHVSAQLERVRVSPQDANPLMANG
 TLTRRHQNGRFVGDADLERQKFSDLKLNGPQD HSHLLYSTIPRMQEPGQIVETYTED
 PEGAMSVVSVETSDDGTTRRTETT VKKVKTVTTRTVQPVAMGPDGLPVDASSVSNNY
 IQTLGRDFRKNGNGGPGPYVGQAGTATLPRNFHYPPDGYSRHYEDGYPGGSDNYGSL
 SRVTRIEERYRPSMEGYRAPSRQDVYGPQPQVRVGGSSVDLHRFHPEPYGLEDDQRS
 MGYDDLDYGMMSDYGTARRTGTPSDPRRRLRSYEDMIGEEVPSDQYYWAPLAQHER
 GSLASLDSL RKGPPPPNWRQPELPEVIAM LGFRLDAVKSNAAAYLQHLCYRNDKVKT
 DVRKLKGIPVLVGLLDHPKKEVHLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRK
 ARDMDLTEVITGTLWNLSSHDSIKMEIVDHALHALTDEVII PHSGWEREPNEDCKPRHIE
 WESVLTNTAGCLRNVSSERSEARRKLRECDGLVDALIFIVQAEIGQKDS DSKLVENCVC
 LLRNLSYQVHREIPQAERYQEAAPNVANNTGPHAASCFGAKKGKGKKPIEDPANDTV D
 FPKRTSPARGYELLFQPEVVRIYISLLKESKTPAILEASAGAIQNL CAGRWTYGRYIRSAL
 RQEKALSAIADLLTNEHERVVKAASGALRNLA VDARNKELIGKHAIPNLVKNLPGGQQNS
 SWNFSEDTVISILNTINEVIAENLEAAKKLRETQGIEKLVLINKSGNRSEKEVR AAALVLQT
 IWGYKELRKPLEKEGWKKSDFQVNLNNASRSQSSHSYDDSTLPLIDRNQKSDKKPDRE
 EIQMSNMGSNTKSLDNNYSTPNERGDHNR TLDRSGDLGDMEPLKGTTPLMQDEGGQES
 LEEELDVLVLDDEGGQVSYP SMQKI

SEQ ID No: 50 (NCadh)

MCRIAGALRTLPLLLALLQASVEASGEIALCKTGFPEDVYSAVLSKDVHEGQPLLNVKF
 SNCNGKRKVQYESSEPADFKVDEDGMVYAVRSFPLSSEHAKFLIYAQDKETQEKWQV
 AVKLSLKPTLTEESVKESAEVEEIVFPRQFSKHSGHLQRQKRDWVIPPINLPENSRRGPPF
 QELVRIRSDRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDREQIARFHLRAH
 AVDINGNQVENPIDIVINVIDMNDNRPEFLHQVWNGTVPEGSKPGTYVMTVTAIDADDP
 NALNGMLRYRIVSQAPSTPSPNMFTINNETGDIITVAAGLDREKVQQYTLLIQATDMEGN
 PTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPENRVDIIVANLTVTDKDQPHTPAWN
 AVYRISGGDPTGRFAIQTDPNSNDGLVTVVKPIDFETNRMFVLTVAAENQVPLAKGIQHP
 PQSTATVSVTIDVNENPYFAPNPKIIRQEEGLHAGTMLTTFTAQDPDRYMQQNIRYTKL
 SDPANWLKIDPVNGQITTI AVL DRESPNVKNNIYNATFLASDNGIPPMMSGTGTLQIYLLDI
 NDNAPQVLPQEAETCETPDPNSINITALDYDIDPNAGPFAFDLPLSPVTIKRNWTITRLNG
 DFAQLNLKIKFLEAGIYEVPIITDSGNPPKSNISILRVKVCQCDSNGDCTDVDRIVGAGLG
 TGAIIALLCIIILLILVLMFVWMKRDRKERQAKQLLIDPEDDVRDNILKYDEEGGGGEEDQ
 DYDLSQLQQPDTVEPDAIKPVGIRRM DERPIHAEPQYPVRS AAPH PGDIGDFINEGLKAA
 DNDPTAPPYDSSLVFDYEGSGSTAGSLSSLNSSSSSGGEQDYDYLDNWGPRFKKLADM
 YGGGDD

SEQ ID No:51 (Reelin)

MERSGWARQTFLALLLGATLRARAAAGYYPRFSPFFFLCTHHGELEGDGEQGEVLISL
 HIAGNPTYYPGQEYHVTISTSTFFDGLLVTGLYTSTSVQASQSIGGSSAFGFGIMSDHQ
 FGNQFMCSVVASHVSHLPTTNLSFIWIAPPAGTGCVNFMATATHRGQVIFKDALAQQLC
 EQGAPTDVTVHPHLAEIHSDSILRDDFDSYHQLQLNPNIWVECNCETGEQCGAIMHG
 NAVTFCEPYGPRELITTGLNTTTTASVLQFSIGSGSCRFSYSDPSIIVLYAKNNSADWIQLE
 KIRAPSNVSTIIHILYPEDAKGENVQFQWKQENLRVGEVYEACWALDNILIINSAHRQVV
 LEDSLDPVDTGNWLFFPGATVKHSCQSDGNSIYFHGNEGSEFNFATTRDVDLSTEDIQE
 QWSEEFESQPTGWDVLGAVIGTECGTIESGLSMVFLKDGGERKLCTPSMDTTGYGNLRF
 YFVMGGICDPGN SHENDI ILYAKIEGRKEHITLDTLSYSSYKVPSLVSVVINPELQTPATKF
 CLRQKNHQGHNRNVWAVDFFHVLPVLPSTMSHMIQFSINLGCPTHQPGNSVSLEFSTN
 HGRSWSLLHTECLPEICAGPHLPSTVYSSENYSGWNRITIPNAALTRNTRIRWRQT
 GPILGNMWAIDNVYIGPSCLKFCSGRGQCTR HGCKCDPGFSGPACEMASQTFPMFISE
 SFGSSRLSSYHNFYSIRGAEVSF GCGVLASGKALVFNKEGRRQLITSFLDSSQS RFLQF
 TLRLGSKSVLSTCRAPDQPGEGVLLHYSYDNGITWKLLEHYSYLSYHEPRIISVELPGDA
 KQFGIQFRWWQPYHSSQREDVWAIDEIIMTSVLFNSISLDFTNLVEVTQSLGFYLG NVQ
 PYCGHDWTLCTGTGDSKLASSMRYVETQSMQIGASYMIQFSLVMGCGQKYTPHMDNQV

KLEYSTNHGLTWHLVQEECLPSMPSCQEFTSASIYHASEFTQWRRVIVLLPQKTWSSAT
RFRWSQSYTAQDEWALDSIYIGQQCPNMCSGHGSCDHGICRCDQGYQGTECHPEA
ALPSTIMSDFENQNGWESDWQEVIGGEIVKPEQGCQGVSSGSSLYFSKAGKRQLVSWD
LDTSWVDFVQFYIQIGGESASCNKPDSREEGVLLQYSNNGGIQWHLLAEMYFSDFSKP
RFVYLELPAAAKTPCTRFRWWQPVFSGEDYDQWAVDDIILSEKQKQIIPVINPTLPQNF
YEKPAFDYPMNQMSVWLMLANEGMVKNETFCAATPSAMIFGKSDGDRFAVTRDLTLK
PGYVLQFKLNIGCANQFSSTAPVLLQYSHDAGMSWFLVKEGCYPASAGKGCEGNSREL
SEPTMYHTGDFEEWTRITIVIPRSLASSKTRFRWQIESSSQKNVPPFGLDGVYISEPCPS
YCSGHGDCISGVCFCDLGYTAAQGTCVSNVPNHNEMFDRFEGKLSPLWYKITGAQVG
TGCGTLNDGKSLYFNGPGKREARTVPLDTRNIRLVQFYIQIGSKTSGITCIKPRTRNEGLI
VQYSNDNGILWHLLRELD FMSFLEPQIISIDLPQDAKTPATAFRWWQPQHKGKHSQAQWA
LDDVLIGMNDSSQTGFQDKFDGSDIDLQANWYRIQGGQVDIDCLSMDTALIFTENIGKPRY
AETWDFHVSASTFLQFEMSMGCSKPFSSNSHSVQLQYSLNNGKDWHLVTEECVPPTIG
CLHYTESSITYTSERFQNWKRITVYLPSTISPRTRFRWQIANYTVGADSWAIDNVVLASG
CPWMCSGRGICDAGRCVCDRGFGGPYCVPVVPLPSILKDDFNGLHPDLWPEVYGAE
RGNLNGETIKSGTSLIFKGEGLRMLISRDLDCNTMYVQFSLRFIAKSTPERSHSILLQFSI
SGGITWHLMDDEFYFPQTTNILFINVPLPYTAQTNATRFRLWQPYNNGKKEEIWIVDDFIID
GNNVNNPVMLLDTFDFGPREDNWWFFYPGGNIGLYCPYSSKGAPEEDSAMVFVSNEVG
EHSITTRDLNVNENTI IQFEINVG CSTDSSSADPVRLEFSRDFGATWHLLLPLCYHSSSH
VSSLCSTEHHPSSTYYAGTMQGWRRREV VHFGLHLCGSVRFRWYQGFYPAGSQPVT
WAIDNVYIGPQCEEMCNGQGSCINGTKCICDPGYSGPTCKISTKNPDFLKDDFEGQLES
DRFLMSGGKPSRKCGILSSGNLFFNEDGLRMLMTRDLDSLHARFVQFFMRLGCGKG
VPDPRSQPVLLQYSLNNGGLSWSLQEF LFSNSSNVGRYIALEIPLKARSGSTRLRWWQ
PSENGHFYSPWVIDQILIGNISGNTVLEDDFTTLD SRKWLLHPGGTKMPVCGSTGDAL
VFIEKASTRYVVSTDVAVNEDSFLQIDFAASCSVT DSCYAIELEYSVDLGLSWHPLVRDC
LPTNVECSRYHLQRILVSDTFNKWTRITLPLPPYTRSQATRFRWHQPAPFDKQQTWAID
NVYIGDGCIDMCSGHGRCIQGNCVCDEQWGGLYCDDPETS LPTQLKDNFN RAPSSQN
WLTVNGGKLSTVCGAVASGMALHFSGGCSRL LVTVDLNL TNAEFIQFYFMYGCLITPNN
RNQGV LLEYSVNGGITWNLLMEIFYDQYSKPGFVNILLPPDAKEIATRFRWWQPRHDGL
DQNDWAIDNV LISGSADQRTVMLDTFSSAPVPQHERSPADAGPVGRIAFDMFMEDKTS
VNEHWLFHDDCTVERFCDSPDGVMLCGSHDGREVYAVTHDLTPTEGWIMQFKISVGC
KVSEKIAQNQIHVQYSTDFGVSWNYLVPQCLPADPKCSGSVSQPSVFFPTKGWKRITY
PLPESLVGNPVRFRFYQKYSMDMQWAIDNFYLGPGCLDNCRGHGDCLREQCICDPGYS
GPNCYLTHTLKTLKERFDSEEIKPDLWMSLEGGSTCTECGILAEDTALYFGGSTVRQA

VTQDLDLRGAKFLQYWGRIGSENNMTSCHRPICRKEGVLLDYSTDGGITWTLLHEMDY
 QKYISVRHDYILLPEDALTNTTRLRWWQPFVISNGIVVSGVERAQWALDNILIGGAEINPS
 QLVDTFDDEGTSHEENWSFYFNAVRTAGFCGNPSFHLYWPNKKKDKTHNALSSRELII
 QPGYMMQFKIVVGCEATSCGDLHSVMLEYTKDARSDSWQLVQTQCLPSSSNSIGCSP
 FQFHEATIYNSVNSSSWKRITQLPDHVSSSATQFRWIKGEETEKQSWAIDHVIYIGEAC
 PKLCSGHGYCTTGAICICDESFQGDDCSVFSHDLPSYIKDNFESARVTEANWETIQGGVI
 GSGCGQLAPYAHGDSLYFNGCQIRQAATKPLDLTRASKIMFVLQIGSMSQTDSCNSDLS
 GPHAVDKAVLLQYSVNNGITWHVIAQHQPDKFTQAQRVSYNVPLEARMKGVLLRWWQ
 PRHNGTGHDQWALDHVEVVLVSTRKQNYMMNFSRQHGLRHFYNNRRRRSLRRYP

SEQ ID No:52 (Sortilin-related receptor)

MATRSSRRESRLPFLFTLVALLPPGALCEVWTQRLHGGSAPLPQDRGFLVVQGDPREL
 RLWARGDARGASRADEKPLRRKRSALQPEPIKVYGGVSLNDSHNQMNVHWAGEKS
 NVIVALARDSLALARPSSDVVYSYDYGKSFKKISDKLNFGNGRSEAVIAQFYHSPADN
 KRYIFADAYAQYLWITFDFCNTLQGFSIPFRAADLLHASKASNLLGFDNRSHPNKQLWKS
 DDFGQTWIMIQEHVKSFSWGIDPYDKPNTIYIERHEPSGYSTVFRSTDFFQSRENQEVIL
 EEVRDFQLRDKYMFATKVHLLGSEQQSSVQLWVVSFGRKPMRAAQFVTRHPINEYYIA
 DASEDQVFVFCVSHSNRTNLYISEAEGKFSLSLENVLYYSPGGAGSDTLVRYFANEPP
 ADFHRVEGLQGVYIATLINGSMNEENMRSVITFDKGGTWEFLQAPFTGYGEKINCELS
 QGCSLHLAQRLSQLLNQLRRMPILSKESAPGLIATGSVGKNLASKTNVYISSSAGARW
 REALPGPHYTTWGDHGGIITAIAQGMETNELKYSTNEGETWKTFFSEKPVFVYGLLTP
 GEKSTVFTIFGSNKENVHSLILQVNATDALGVPCTENDYKLWSPSDERGNECLLGHKT
 VFKRRTPHATCFNGEDFDRPVVVSNCSTREDYECDFGFKMSDLSLEVCVPDPEFSG
 KSYSPVPVPCVPGSTYRRTRGYRKISGDTCSGGDVEARLEGELVPCPLAEENEFILYAVR
 KSIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQRLCLNGSTGQEVI
 INSGLETVEALAFEPLSQLLYWVDAGFKKIEVANPDGDFRLTIVNSSVLDRPRALVLVPQ
 EGVMFWTDWGDLPKGIYRSNMDGSAAYHLVSEDKWPNGISVDDQWIYWTDAYLECI
 ERITFSGQQRSVILDNLPHPYAIAVFKNEIYWDWSQLSIFRASKYSGSQMEILANQLTG
 LMDMKIFYKGKNTGSNACVPRPCSLCLPKANNRSRSCRPEDVSSSVLPSGDLMCDP
 QGYQLKNNTCVKEENTCLRNQYRCSNGNCINSIWWCDFDNDCGDMSDERNCPTTICD
 LDTQFRQCESGTCIPLSYKCDLEDDCGDNDSESHCEMHQCRSDEYNCSSGMCISSW
 VCDGDNDCRDWSDEANCTAIYHTCEASNQCRNGHCIPQRWACDGDTCQDGSDED
 PVNCEKKCNGFRCPNGTCIPSSKHCDGLRDCSDGSDEQHCEPLCTHFMDFVCKNRQQ
 CLFHSMVCDGIIQCRDGSDEDAAFAGCSQDPEFHKVCDEFQFQCQNGVCISLIWKCDG

MDDCGDYSDEANCENPTEAPNCSRYFQFRCENGHCIPNRWKCDREND CGDWSDEKD
 CGDSHILPFSTPGPSTCLPNYYRCSSGTCVMDTWVCDGYRDCADGSDEEACPLL ANV
 TAASTPTQLGRCDRFEFECHQPKTCIPNWKRCQDGHQDCQDGRDEANCPTHSTLTCMS
 REFQCEEDGEACIVLSERC DGFDCSDESDEKACSD ELTVYKVQNLQWTADFSGDVTLT
 WMRPKKMPSASC VYNVYYRVVGESIWKTLETHSNKTNTVLKVLKPDTTYQVKVQVQCL
 SKAHNTNDFVTLRTPEGLPDAPRNLQLSLPREAEGVIVGHWAPPIHTHGLIREYIVEYSR
 SGSKMWASQRAASN FTEIKNLLVNTLYTVRVA AVTSRGIGNWSDSKSITTIGKGVIPPPDI
 HIDSYGENYLSFTLT MESDIKVNGYVVNLFWAFDTHKQERRTLNFRGSILSHKVGNLTA
 HTSYEISAWAKTDLGDSPLAFEHVMTRGVRPPAPSLKAKAINQTAVECTWTGPRNVVY
 GIFYATSFLDLYRNPKSLTTSLHNKTVIVSKDEQYLFLVRVVVPYQGPSSDYVVVKMIPD
 SRLPPRHLHVHTGKTSVVIKWESPYDSPDQDLLYAI AVKDLIRKTD RSYKVKSRNSTVE
 YTLNKLEPGGKYHIIVQLGNMSKDSSIKITTVSLSAPDALKIITENDHVLLFWKSLALKEKH
 FNESRGYEIHMFD SAMNITAYLGNTTDNFFKISNLKMGHNYTFTVQARCLFGNQICGEP
 AILLYDELGSGADASATQAARSTDVA AVVPILFLILLSLGVGFAILYTKHRRRLQSSFTAFA
 NSHYSSRLGSAIFSSGDDLGEDDEDAPMITGFSDDVPMVIA

SEQ ID No:53 (18 kDa microsomal signal peptidase subunit)

MLSLDFLDDVRRMKNRQLYYQVLNFGMIVSSALMIWKGLMVITGSESPIVVVLSGSMEP
 AFHRGDLLFLTNRVEDPIRVGEIVVFRIEGREIPIVHRVLKIHEKQNGHIKFLT KGDNNAVD
 DRGLYKQGQHWLEKKDVVGRARGFVPYIGIVTILMNDYPKF KYAVLFLLGLFVLVHRE

SEQ ID No: 54 (CLGN)

HLPKQQRGGVCLGVKSKWQPKLRTGREKIINMHFQAFWLCLGLLFISINAEFMDDDVET
 EDFEENSEEIDVNESELSSEIKYKTPQPIGEVYFAETFDSGRLAGWVLSKAKKDDMDEEI
 SIYDGRWEIEELKENQVPGDRGLVLKSRAKHH AISAVLAKPFIFADKPLIVQYEVNFQDGI
 DCGGAYIKLLADTDDLILENFYDKTSYIIMFGPDKCGEDYKLHFIFRHKHPKTGVFEEKHA
 KPPDVDLKKFFTDRKTHLYTLVMNPDDT FEVLVDQTVVNKGSLL EDVVPPIKPPKEIEDP
 NDKKPEEWDERAKIPDPSAVKPEDWDESEPAQIEDSSVVKPAGWLDDEPKFIPDPNAE
 KPDDWNEDTDGEWEAPQILNPACRIGCGEWKPPMIDNPKYKGVWRPPLVDNPNYQGI
 WSPRKIPNP DYFEDDHPFLT SF SALGLELWSMTSDIYFDNFIICSEKEVADHWAADGW
 RWKIMIANANKPGVLKQLMAAAEGHPWLWLIYLV TAGVPIALITSFCWPRKVKKKHKDT
 EYKKT DICIPQTKGVLEQEEKEEKA ALEKPM DLEEEKKQNDGEMLEKEEESEPEEKSEE
 EIEIIEGQEE SNQSNKSGSEDEMKEADESTGSGDGPIKSVRKRRVRKD

SEQ ID No:55 (ECSIT)

MSWVQATLLARGLCRAWGGTCGAALTGTSISQVPRRLPRGLHCSAAAHSSSEQSLVPS
 PPEPRQRPTKALVPFEDLFGQAPGGERDKASFLQTVQKFAEHSVRKRGHIDFIYLALRK
 MREYGVERDLAVYNQLLNIFPKEVFRPRNIIQRIFVHYPRQQEAGIIVLEQMENHGVMP
 NKETEFLLIQIFGRKSYPMKLKLVRLKLWFPRFMNVNPFVPRDLPQDPVELAMFGLRHM
 EPDLSARVTIYQVPLPKDSTGAADPPQPHIVGIQSPDQQAALARHNPARPVFVEGPFSL
 WLRNKCYYYHILRADLLPPEEREVEETPEEWNLYYPMQLDLEYVRSGWDNYEFDINEV
 EEGPVFAMCMAGAHDQATMAKWIQGLQETNPTLAQIPVVFRLAGSTRELQTSSAGLEE
 PPLPEDHQEEDDNLQRQQGQS

SEQ ID No:56 (FLJ20342)

MPSASCDTLLDDIEDIVSQEDSKPQDRHFVRKDVVPKVRRRNTQKYLQEEENSPPSDS
 TIPGIQKIWIRTWGCSHNNSDGEYMAGQLAAYGYKITENASDADLWLLNSCTVKNPAED
 HFRNSIKKAQEENKKIVLAGCVPQAQPRQDYLKGLSIIGVQQIDRVVEVVEETIKGHSVR
 LLGQKKDNGRRLGGARLDLPKIRKNPLIEIISISTGCLNACTYCKTKHARGNLA SYPIDEL
 VDRAKQSFQEGVCEIWLTS EDTGAYGRDIGTNLPTLLWKLVEVIPEGAMLRLGMTNPPY
 ILEHLEEMAKILNHPRVYAFLHIPVQSASDSVLMEMKREYCVADFKRVVDFLKEKVPGITI
 ATDIICGFPGETDQDFQETVKLVEEYKFPSLFINQFYPRPGTPAAKMEQVPAQVKKQRT
 KDLSRVFHSYSPYDHKIGERQQVLVTEESFDSKFYVAHNQFYEQVLVPKNPAFMGKMV
 EVDIYESGKHFMKGQPVSDAKVYTPSISKPLAKGEVSGLTKDFRNGLGNQLSSGSHTSA
 ASQCDSASSRMVLPMPRLHQDCALRMSVGLALLGLLFAFFVKVYN

SEQ ID No:57 (KIAA0090)

MAAEWASRFLWATLLIPAAAVYEDQVGKFDWRQQYVGKVKFASLEFSPGSKKLVA
 TEKNVIAALNSRTGEILWRHVDKGTAE GAVDAMLLHGQDVITVSNGGRIMRSWETNIGG
 LNWEITLDSGSFQALGLVGLQESVRYIAVLKKTTLALHHLSSGHLKWVEHLPESDSIHYQ
 MVYSYSGSVVWALGVVPF SHVNIVKFNVEDGEIVQQVRVSTPWLQHLSGACGVVDEA
 VLVCPDPSSRSLQTLALET EWELRQIPLQSLDLEFGSGFQPRVLPTQPNPVDASRAQFF
 LHLSPSHYALLQYHYGTLSLLKNFPQTALVSFATTGEKTVAAVMACRNEVQKSSSSSEDG
 SMGSFSEKSSSKDSLACFNQTYTINLYLVETGRRLD TTITFSLEQSGTRPERLYIQVFLK
 KDDSVGYRALVQTEDHLLLFLQQLAGKVVLWSREESLAEVVCLEMVDLPLTGAQAELE
 GEFGKKADGLLGMFLKRLSSQLILLQAWTSHLWKMFYDARKPRSQIKNEINIDTLARDEF
 NLQKMMVMVTASGKLFGIESSSGTILWKQYLPNVKPDSSFKLMVQRTTAHFPHPPQCT
 LLVKDKESGMSSLYVFNPIFGKWSQVAPPVLKRPIQLSLLPVMDQDYAKVLLIDDEYK

VTAFPATRNVLRQLHELAPSIFFYLVDAEQGRLCGYRLRKDLTTELSWELTIPPEVQRIV
 KVKGKRSSEHVHSQGRVMGDRSVLYKSLNPNLLAVVTESTDAHHERTFIGIFLIDGVTG
 RIIHSSVQKKAKGPVHIVHSENWVVYQYWNTKARRNEFTVLELYEGTEQYNATAFSSLD
 RPQLPQVLQQSYIFPSSISAMEATITERGITSRHLLIGLPSGAILSLPKALLDPRRPEIPTEQ
 SREENLIPYSPDVQIHAERFINYNQTVSRMRGIYTAPSGLESTCLVVAYGLDIYQTRVYP
 SKQFDVLKDDYDYVLISSVLFGLVFATMITKRLAQVKLLNRAWR

SEQ ID No:58 (NICE-3)

MASGSNWLSGVNVVLVMAYGSLVFVLLFIFVKRQIMRFAMKSRRGPHVPVGHNAPKDL
 KEEIDIRLSRVQDIKYEPQLLADDDARLLQLETQGNQSCYNYLYRMKALDAIRTSEIPFHS
 EGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLLDGYETARYGTGVFGQNEYLR
 YQEALSELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVTYLPSSQKSKRAKHFL
 ELKSFKDNYNTLESTL

SEQ ID No: 59 (CK2B)

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEP
 DEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQ
 PMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYR
 PKRPANQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTIR

SEQ ID No: 60 (PTP LOC114971)

MAATALLEAGLARVLFYPTLLYTLFRGKVPGRAHRDWYHRIDPTVLLGALPLRSLTRQLV
 QDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTGIPTLDNLQKGVQFA
 LKYQSLGQCVYVHCKAGRSRSATMVAAYLIQVHKWSPEEAVRAIAKIRSYIHIRPGQLDV
 LKEFHKQITARATKDGTFVISKT

SEQ ID No: 61 (STT3)

MTKFGFLRLSYEKQDTLLKLLILSMAAVLSFSTRLFAVLRFESVIHEFDPYFNRYRTTRFLA
 EEGFYKFHNWFDDRAWYPLGRIIGGTIYPGLMITSAAIYHVLHFFHITIDIRNVCVFLAPLF
 SSFTTIVTYHLTKELKDAGAGLLAAAMIAVVPGYISRSVAGSYDNEGIAIFCMLLTYYMWI
 KAVKTGSICWAAKCALAYFYMVSSWGGYVFLINLIPLHVLVLMLTGRFSHRIYVAYCTVY
 CLGTILSMQISFVGFPVLSSEHMAAFGVFGLCQIHAFVDYLRSKLNPQQFEVLFRSVIS
 LVGFVLLTVGALLMLTGKISPWTGRFYSLLDPSYAKNNIPIIASVSEHQPTTWSSYYFDLQ
 LLVFMFPVGLYYCFSNLSDARIFIIMYGVTSMYFSAVMVRLMLVLAPVMCILSGIGVSQVL

STYMKNLDIRPDKKSKKQQDSTYPIKNEVASGMILVMAFFLITYTFHSTWVTSEAYSSP
 SIVLSARGGDGSRIIFDDFREAYYWL RHNTPEDAKVMSWWDYGYQITAMANRTILVDNN
 TWNNTHISRVGQAMASTEELKAYEIMRELDVSYVLVIFGGLTGYSSDDINKFLWMVRIGG
 STDTGKHIKENDYYTPTGEFRVDREGSPVLLNCLMYKMCYYRFGQVYTEAKRPPGFDR
 VRNAEIGNKDFELDVLEEAYTTEHWLVRIYKVKDLDNRGLSRT

SEQ ID No: 62 (NicAChRa3)

MGSGPLSLPLALSPRLLLLLLLLSLLPVARASEAEHRLFERLFEDYNEIIRPVANVSDPVII
 HFEVMSQLVKVDEVNQIMETNLWLKQIWN DYKLKWNPSDYGGAEFMRVPAQKIWKP
 DIVLYNNAVGD FQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGS
 WSYDKAKIDLVLIGSSMNLKDYWESGEWAIKAPGYKHDIKYNCCEEIYPDITYSLYIRRL
 PLFY TINLIIPCLLISFLT VLVFYLP SDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEY
 LLFTMIFVTL SIVITV FVLNVHYRTPTTHTMP SWVKTVFLNLLPRVMFMTRPTSNEGNAQ
 KPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGYCHHRIKISNFSANLTRSSSS
 ESVDVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEEQKAQEIQQLKRKEKSTETSDQ
 EPGL

SEQ ID No: 63 (SLC4A2)

MSSAPRRPAKGADSFCTPEPESLGPGTGPFP EQEDELHRTLGV FEFEEILQEAGSRG
 GEEPGRSYGEEDFEYHRQSSHIIHPLSTHLPPDARRRKTPQGPGRKPRRRPGASPT
 GETPTIEEGEEDEDEASEAEGARALTQPSPVSTPSSVQFFLREDD SADRKAERTSPSSP
 APLPHQEATPRASKGAQAGTQVEEA EAEAVAVASGTAGGDDGGASGRPLPKAQPGHR
 SYNLQERRRIGSMTGAEQALLPRVPTDEIEAQT LATADLDMKSHRFEDVPGVRRHLVR
 KNAKGSTQSGREGREPGTPRARPRAPHKPHEVFVELNELLLDKNQEPQWRETARWI
 KFEEDVEEETERWGKPHVASLSFRSLELRLRLAHGAVLLDLDQQTLP GVAHQVVEQM
 VISDQIKAEDRANVLRALLLKHSHPSDEKDFSFRNISAGSLGSLLGHHHGQGAESDPH
 VTEPLMGGVPETRLEVERERDVPPPAPPAGITRSKSKHELKLEKIPENAEATVVLVGCV
 EFLSRPTMAFVRLREAVELDAVLEVPVPVRFLFLLGPSSANMDYHEIGRSISTLM SDKQ
 FHEAAYLADEREDLLTAINAFLDCSVLPPSEVQGEELLRSVAHFQRQMLKKREEQGRL
 LPTGAGLEPKSAQDKALLQMVEAAGAAEDDPLRRTGRPFGLIRDVRRRYPHYLSDFR
 DALDPQCLA AVIFIYFAALSPAITFGG LLGEKTQDLIGVSELIMSTALQGVVFC LLGAQPLL
 VIGFSGPLLVFEEAFFSFCSSNHLEYLVGRVWIGFWLVFLALLMVALEGSFLVRFVSRFT
 QEIFAFLISLIFIYETFYKLVKIFQEHLHGCSASNSSEVDGGENMTWAGARPTLGPGNR
 SLAGQSGQGKPRGQPNTALLSLVLMAGTFFIAFFLRKFKNRFFPGRIRRVIGDFGVPIAI

LIMVLVDYSIEDTYTQKLSVPSGFSVTAPEKRGWVINPLGEKSPFPVWMMVASLLPAILV
 FILIFMETQITTLISKKERMLQKSGSFHLDLLLIVAMGGICALFGLPWLAATVRSVTHAN
 ALTVMSKAVAPGDKPKIQEVKEQRTVGLLVALLVGLSIVIGDLLRQIPLAVLFGIFLYMGVT
 SLNGIQFYERLHLLLMPPKHHPDVTYVKKVRTLRMHLFTALQLLCLALLWAVMSTAASLA
 FPFILILTVPLRMVVLTRIFTDREMKCLDANEAEPVFDEREGVDEYNEMPMPV

SEQ ID No: 64 (HIFPH3/EGLN3)

MGKGGNQGEAAEREVSVP TFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQ
 RVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALR
 KTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL
 QHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNM
 LHVFLGEWQPIEYGKKKLKYPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIVHKNWVDL
 AWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQMNHIVMEIDQEAYRDWFS
 SQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNLHKKIAPLVKSLCAKHGIEYQE
 KPLLRALLDIIRSLKKSGKLWLDAYLHK

SEQ ID No:65 (STX10)

MSLEDPPFFVVRGEVQKAVNTARGLYQRWCELLQESAAGVGRELDWTTNELRNGLSIE
 WDLEDLEETIGIVEANPGKFKLPAGDLQERKVFVERMREAVQEMKDHMVSP TAVAFLE
 RNNREILAGKPAAQKSPSDLLDASAVSATSRYIEEQQATQQQLIMDEQDQQLEMVSGSIQ
 VLKHMSGRVGEELDEQGIMLDFAQEMDHTQSRMDGVLRKLAKVSHMTSDRRQWCAI
 AVLVGVL LLLVL LLLFSL

SEQ ID No:66 (Presenilin-2)

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQNEEDG
 EEDPD RYVCSGVPGRPPGLEEEELTKYGAKHVIMLFVPVTLCMIVVATIKSVRFYTEKN
 GQLIYTPFTEDTPSVGQRLLNSVLNLTLMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLM
 LLFLFTYIYLGEVLKTYNVAMDYPTLLLTWVNF GAVGMVCIHWKGPLVLQQAYLIMISAL
 MALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV
 WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEE
 ERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLAVFKKALPALPI
 SITFGLIFYFSTDNLVRPFMDTLASHQLYI

SEQ ID No:67 (Wolframin)

MDSNTAPLGPSCPQPPAPQPQARSRLNATASLEQERSERPRAPGPQAGPGPGVRDA
 AAPAEPQAQHTRSREERADGTGPTKGDMEIPFEEVLERAKAGDPKAQTEVGKHYLQLAG
 DTDEELNSCTAVDWLVLAQKGRREAVKLLRRCLADRRGITSENEREVRQLSSETDLE
 RAVRKAALVMYWKLNPKKKKKQVAVAELENVGQVNEHDGGAQPGPVPKSLQKQRRML
 ERLVSSESKNYIALDDFVEITKKYAKGVIPSSFLQDDEDDDELAKSPEDLPLRLKVVKY
 PLHAIMEIKEYLIDMASRAGMHWLSTIIPTHHINALIFFFIISNLTIDFFAFFIPLVIFYLSFISM
 VICTLKVFQDSKAWENFRTLTDLLLRFEPNLDVEQAEVNFNGWNHLEPYAHFLLSVFFVIF
 SFPIASKDCIPCSELAVITGFFTTSYLSLSTHAEPYTRRALATEVTAGLLSLLPSMPLNW
 PYLKVLGQTFITVPVGHLLVNLVSVPCLLYVYLLYLFFRMAQLRNFKGTYCYLVPYLVCF
 MWCELSVVILLESTGLGLLRASIGYFLFLFALPILVAGLALVGVLQFARWFTSLELTKIAVT
 VAVCSVPLLLRWWTKASFVVGMMVKSLTRSSMVKLILVWLTAIVLFCWFYVYRSEGMKV
 YNSTLTWQQYGALCGPRAWKETNMARTQILCSHLEGHRVTWTGRFKYVRVTDIDNSA
 ESAINMLPFFIGDWMRCLYGEAYPACSPGNTSTAEELCRLKLLAKHPCHIKKFDYKF
 EITVGMPFSSGADGSRSSREEDDVTKDIVLRASSEFKSVLLSLRQGSLEFSTILEGRLGSK
 WPVFELKAISCLNCMAQLSPTRRHVKIEHDWRSTVHGAVKFAFDFFFFPFLSAA

SEQ ID No:68 (BACE1)

MAQALPWLLLWMGAGVLPAGHTQHGIRLPLRSGLGGAPLGLRLPRETDEEPEEPGRR
 GSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQ
 RQLSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGS
 NWEGLGLAYAEIARPDDSLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGG
 SMIIGGIDHSlyTGSlyWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTN
 LRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT
 NQSFRITILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI
 GFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMTIAYVMAAICALFMLP
 LCLMVCQWRCLRLRQQHDDFADDISLLK

SEQ ID No:69 (FLJ30668)

MELHYLAKKSNQADLCDARDWSSRGLPGDQADTAATRAALCCQKQCASTPRATEMEG
 SKLSSSPASPSSSLQNSTLQPDADFPPGLLHSGNNQITAERKVCNCCSQELETSTFTYVDK
 NINLEQRNRSSPSAKGHNHPGELGWENPNEWSQEAASLISEEEDDTSSEATSSGKSID
 YGFISAILFLVTGILLVIISYIVPREVTVDPNNTVAAREMERLEKESARLGAHLDRCVIAGLCL
 LTLGGVILSCLLMMSMWKGElyRRNRFASSKESAKLYGSFNFRMKTSTNENTLELSLVE
 EDALAVQS

SEQ ID No:70 (BSCv protein)

MSEADGLRQRRPLRPQVVTTDDDGQAPEAKDGSSFSGRVFRVTFLLMLAVSLTVPLLGA
 MMLLESPIDPQPLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAHIGDVMFTGTA
 DGRVVKLENGEIIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYKGLFEVN
 PWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEGTD
 DGRILLEVDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGA
 DLFVENMPGFPDNIRPSSSSGGYWVGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFSQET
 VMKFVPRYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLVYLGSRSPFLCRLS
 LQAV

SEQ ID No:71 (FLJ39249)

MAPRPLGPLVLALGGAAAVLGSVLFILWKTYFGRGRERRWDRGEAWWGAEAAARLPEW
 DEWDPEDEEDEEPALEEELEQREVLVLGLDGAGKSTFLRVLSGKPPLEGHIPTWGFNSV
 RLPTKDFEVDLLEIGGSQNLRFYWKEFVSEVDVLVFFVDSADRLRLPWARQELHKLLDK
 DPDLPVVVVANKQDLSEAMSMGELQRELGLQAIDNQREVFLLAASIAPAGPTFEETPGTV
 HIWKLLLELLS

SEQ ID No:72 (Cgl-13)

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEIL
 GVLNSSSRFYHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
 WKLGDPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTD
 ILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSEN
 TLIQQEVDAALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATI
 NIVFDRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAI
 SSKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVS
 ALSSILFLYLAHKQAPEKQMAP

SEQ ID No:73 (ITCH)

MSDSGSQLGSMGSLTMKSQQLQITVISAKLKENKKNWFGSPYVEVTVDGQSKKTEKCN
 NTNSPKWKQPLTVIVTPVSKLHFRVWSHQTLKSDVLLGTAALDIYETLKSNNMKLEEVV
 VTLQLGGDKEPTETIGDLSICLDGLQLESEVVTNGETTCSENGVSCLPRLECNSAISAH
 CNLCLPGLSDSPISASRVAGFTGASQNDGSRSKDETRVSTNGSDDPEDAGAGENRR
 VSGNNSPSLSNGGFKPSRPPRPSRPPPTPRRPASVNGSPSATSESDGSSTGSLPPTN

TNTNTSEGATSGLIPLTISGGSGPRPLNPVTQAPLPPGWEQRVDQHGGRVYYVDHVEKR
 TTWDRPEPLPPGWERRVDNMGRYYYYDHFTRTTTWQRPTLESVRNYEQWQLQRSQL
 QGAMQQFNQRFIYGNQDLFATSQSKEFDPLGPLPPGWEKRTDSNGRVYFVNHNTRIT
 QWEDPRSQGQLNEKPLPEGWEMRFTVDGIPYFVDHNRRTTTYIDPRTGKSALDNGPQI
 AYVRDFKAKVQYFRFWCQQLAMPQHKITVTRKTLFEDSFQQIMSFSPQDLRRRLWVIF
 PGEGLDYGGVAREWFFLLSHEVLNPMYCLFEYAGKDNVCLQINPASYINPDHLKYFRF
 IGRFIAMALFHGKFIDTGFSLPFYKRILNKPVGLKDLESIDPEFYNSLIWVKENNIEECDLE
 MYFSVDKEILGEIKSHDLKPNGGNILVTEENKEEYIRMVAEWRLSRGVVEEQTAFFEGF
 NEILPQQYLQYFDAKELEVLLCGMQEIDLNDWQRHAIYRHYARTSKQIMFWFWQFVKEID
 NEKRMRLQLQFVTGTCRLPVGGFADLMGSNGPQKFCIEKVGKENWLPRSHTCFNRLDLP
 PYKSYEQLKEKLLFAIEETEGFGQE

SEQ ID No:74 (Casein kinase III beta chain)

MSSSEEVSWISWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYRQALDMILDLEP
 DEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQ
 PMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYR
 PKR PANQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTIR

SEQ ID No:75 (Cathepsin B)

MWQLWASLCCLLVLANARSRPSFHPVSDELVNYVNKRNTTWQAGHNFYNVDMSYLKR
 LCGTFLGGPKPPQRMFTEDLKLPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVE
 AISDRICHTNAHVSVEVSAEDLLCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLY
 ESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYS
 VSNSEKDIMAIEYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGGHAIIRILGWGVEN
 GTPYWLANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTDQYWEKI

SEQ ID No:76 (Delta-6 fatty acid desaturase)

MKGKGNQGEAAEREVSVP TFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQ
 RVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALR
 KTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL
 QHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNM
 LHV FVLGEWQPIEYGGKKLKYLPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIVHKNWVDL
 AWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQMNHIVMEIDQEAYRDWFS

SQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNHKKIAPLVKSLCAKHGIEYQE
KPLLRAALLDIIRSLKKSGKLWLDAYLHK

SEQ ID No:77 (Nogo-A)

MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERK
PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSST
VPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPA
APKRRGSSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETA
SLPSLSPLSAAAFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSE
LEYSEMGSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTKLVK
EDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIE
SNLESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAT
ESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTD
NLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYP
AAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHE
PENPPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPD
FSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLVKEST
ETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQM
EELSTAVYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVS
HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLPPDV
SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKK
TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPFRAYLES
EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT
LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE

SEQ ID No:78 (PDGFRB)

MRLPGAMPALALKGELLLLLSLLLLLLEPQISQGLVVTTPGPELVNVSTFVLTCSGSAPV
VWERMSQEPPQEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLETDERKRLYI
FVPDPTVGFLPNDAEELFIFLTEITEITIPCRVTDQPQLVVTLHEKKGDVALPVPYDHQGRF
SGIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSNAVQTVVRQGENITLMCIVIGN
EVVNFETYPRKESGRLVEPVTDFFLDMPYHIRSILHIPSALAELEDSTYTCNVTESVNDH
QDEKAINITVVESGYVRLLGEVGTQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGD
SSAGEIALSTRNVSETRYVSELTIVRVKVAEAGHYTMRAFHEDAQVLSFQLQINVPVR
VLELSESHPDSEGTQVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEESQL

ETNVTYWEEEEEQEFVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEIVVPHSLPFKVVI
 SAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRD
 QLVLGRTLGSAGFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMS
 HLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSKRRPPSAELY
 SNALPVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMA
 PYDNYVPSAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARN
 VLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGIL
 LWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPF
 SQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSSVLYT
 AVQPNEGDNDYIIPDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEPQDEP
 EPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL

SEQ ID No:79 (ENSG00000144840)

MASLDRVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEE
 KTCYIELWDVGGSVGSASSVKSTRAVFYNSVNGIIFVHDLTNKKSSQNLRRWSLEALNR
 DLVPTGVLVTNGDYDQEQFADNQIPLLIGTKLDQIHETKRHEVLTTTAFLAEDFNPEEIN
 LDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRFGAGTLKSLHYD

SEQ ID No:80 (PTK7)

MGAARGSPARPRRLPLLSVLLLPLGGTQTAIVFIKQPSSQDALQGRRALLRCEVEAPG
 PVHVVWLLDGAPVQDTERRFAQGSSLSFAAVDPLQDSGTFQCVARDDVTGEEARSAN
 ASFNIKWIEAGPVVLKHPASEAEIQPQTQVKLRCHIDGHPRPTYQWFRDGTPLSDGQSN
 HTVSSKERNLTLRPAGPEHSGLYSCCAHSASFQACSSQNFTLSIADESFARVVLAPQDV
 VVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATVFANGSLLLTQVR
 PRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGSEERVTCCLPPKGLPEPS
 VWEHAGVRLPTHGRVYQKGHELVLANIAESDAGVYTCHAAANLAGQRRQDVNITVATV
 PSWLKKPQDSQLEEGKPGYLDCLTQATPKPTVWYRNQMLISEDSEVFKNGTLRIN
 SVEVYDGTWYRCMSSTPAGSIEAQAVLQVLEKLKFTPPPQQQCMGFDKEATVPCSAT
 GREKPTIKWERADGSSLPWVTDNAGTLHFARVTRDDAGNYTCIASNGPQQGQIRAHVQ
 LTVAVFITFKVEPERTTVYQGHTALLQCEAQGDPKPLIQWKGKDRILDPTKLGPRMHIFQ
 NGS�VIHDVAPEDSGRYTCIAGNSCNIKHTEAPLYVVDKPVPEESEGGSPPPYKMIQTI
 GLSVGAAYAYIIAVLGLMFYCKKRCKAKRLQKQPEGEPEMECLNGGPLQNGQPSAEI
 QEEVALTSLGSGPAATNKRHSTSDKMHFPRSSLQPITTLGKSEFGEVFLAKAQGLEEGV
 AETLVLVKSLQSKDEQQQLDFRRELEMFGKLNHANVVRLLGLCREAEPHYMVLEYVDL

EDLKQFLRISKSKDEKLKSQPLSTKQKVALCTQVALGMEHLSNNRFVHKDLAARNCLVS
 AQRQVKVSALGLSKDVYNSEYYHFRQAWVALRWMSPEAILEGDFSTKSDVWASGVLM
 WEVFTHGEMPHGGQADDEVLADLQAGKARLPQPEGCPSKLYRLMQRCWALSPKDRP
 SFSEIASALGDSTVDSKP

SEQ ID No:81 (FLJ13977)

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDE
 RRYLNAKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLSVLNRTPTHLIREIILVDDF
 SNPDDDCKQLIKLPVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQP
 LLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQKARRLDP
 TEPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFRVWMCGGSLEIVPCSRV
 GHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKRYYYAARPFALERPFGNVESRL
 DLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQANGTTGSSGQRPAG
 GTSEIWVQKPRVRNRRHAAPQGFDPGAKPSQHWRRPEHPAAE

SEQ ID No:82 (FLJ20481)

MFFSMGFIVAVKGKIASPLEAPVFVAAPHSTFFDGIACVVAGLPSMVSARNENAQVPLIGR
 LLRAVQPVLVSRVDPDSRKNTINEIIRKRTSGGEWPQILVFPEGTCTNRSCITFKPGAFI
 PGVPVQPVLLRYPNKLDTVTWTWQGYTFIQLCMLTFCQLFTKVEVEFMPVQVPNDEEK
 NDPVLFANKVRNLMAEALGIPVTDHTYEDCRLMISAGQLTLPMEAGLVEFTKISRKLKLD
 WDGVRKHLDEYASIASSSKGGRIGIEEFAKYLKLPVSDVLRQLFALFDRNHDGSIDFREY
 VIGLAVLCNPSNTEEIQVAFKLFVDVEDGYITEEEFSTILQASLGVPDLDVSGLFKEIAQG
 DSISYEEFKSFALKHPEYAKIFTTYLDLQTCHVFSLPKEVQTTPTASNKVSPEKHEESTS
 DKKDD

SEQ ID No:83 (SERPINA1)

MPSSVSWGILLLAGLCCLVPVSLAEDPQGDAQAQKTDTSHHQDQDHPTFNKITPNLAFAF
 SLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTETPEAQIHEGF
 QELLRTLNPDSQLQLTTGNGLFLSEGLKLVDFLEDVKKLYHSEAFTVNFGDTEEAKE
 QINDYVEKGTQGKIVDLVKELDRDVFALVNYIFFKGKWERPFVVDTEEDFHVDQVT
 TVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITK
 FLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAAPLKLSKAVH
 KAVLTIDEKGTAAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK

SEQ ID No:84 (FLJ22390)

MRPRRPHQIADLFRPKDQIAYS DTS PFLILSEASLADLNSRLEKKVKATNFRPNIVISGCD
VYAEDSWDELLIGDVELKRVMACSRCILTTVDPDTGVMSRKEPLETLKSYRQC DP SERK
LYGKSPLFGQYFVLENPGTIKVGD PVYLLGQ

SEQ ID No:85 (SIM TO Y71H10A. 2.P.)

MVSIPEYYEGKNVLLTGATGFLGKV LLEKLLRSCPKN SVYVLVRQKAGQTPQERVEEV
LSGKLFDRLRDENPDFREKIIAINSELTQPKLALSEEDKEVIIDSTNIIFHCAATVRFNENLR
DAVQLNVIATRQLILLAQQMKNLEVF MHVSTAYAYCNRKHIDEVVYPPPVDPKKLIDSLE
WMDDGLVNDITPKLIGDRPNTYIYTKALAEYV VQQEGAKLNVAIVRPSIVGASWKEPFPG
WIDNFNGPSGLFIAAGKGILRTIRASNNALADLPVDV VVNMSLAAAWYSGVNRPRNIM
VYNCTTGSTNPFHWGEVEYHVISTFKRNP LEQA FRRPNVNLTSNHLLYHYWIAVSHKAP
AFLYDIYLRMTGRSPRCPSPFKFNSNSLSHHYRKGVSHRVSALLLDCTHVDRSETATFNI
DVRQLHWA EYIENYCLGTKKYVLNEEMSGLP AARKHLNKT LFSLFHTALCHGKLT FVDD
TFGFPCLLASGGP LLSVSLHFSAYVYSQIHLAFILRDLGSHSAPSLASLAGPRELTVGSLL
DREWRQIKTDDFELGKSAGEVDLEGADIEGCLLATSPAVRQQALLQRGVQWYISIPTTQ
ETVAMEMQI

SEQ ID No:86 (Hypothetical protein tyrosine phosphatase *ensg00000149185*)

MAATALLEAGLARVLFYPTLLYTLFRGKVP GRAHRDWYHRIDPTVLLGALPLRSLTRQLV
QDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTG IPTLDNLQKGVQFA
LKYQSLGQC VYVHCKAGRSRSATMVAAYLIQVHKWSPEEAVRAIAKIRSYIHIRPGQLDV
LKEFHKQITARATKDGT FVISKT

SEQ ID No:87 (ICAM-2)

MSSFGYRTLTV ALFTLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGG
LETSLNKILLDEQAQWKHYLVSNISHDTV LQCHFTCSGKQESMNSNVSVYQPPRQVILT
LQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNST
ADREDGHRNFSCLA VL DLM SRGGNIFHKHSAPKM LEIYEPVSDSQMVII VTVVSVLLSLF
VTSVLLCFIFGQHLRQQRMGT YGVRAAWRRLPQA FRP

SEQ ID No:88 (KIAA1181)

ASGEWRVSGGRPAGAGRPEEALAAGSDPRGAAARLACSAPTGGGTMPFD FRRFDIY
RKVPKDLTQPTYTGAIISICCLFILFLFLSELTGFITTEVVNELYVDDPDKDSGGKIDVSLN

ISLPNLHCELVGLDIQDEMGRHEVGHIDNSMKIPLNNGAGCRFEGQFSINKVPGNFHVS
 THSATAQPQNPDMTHTVHKLSFGDTLQVQNIHGAFNALGGADRLTSNPLASHDYILKIVP
 TVYEDKSGKQRYSYQYTVANKEYVAYSHTGRIIPAIWFRYDLSPITVKYTERRQPLYRFIT
 TICAIIGGTFTVAGILDSCIFTASEAWKKIQLGKMH

SEQ ID No:89 (KIAA1533)

NSKKMQSWYSMLSPTYKQRNEDFRKLFSLPEAERLIVDYSCALQREILLQGRLYLSEN
 WICFYSNIFRWETTISIQLKEVTCLKKEKTAKLIPNAIQICTESEKHFFTSFGARDRCFLIF
 RLWQNALLEKTLSPRELWHLVHQCYGSELGLTSEDEDYVSPLQLNGLGTPKEVGDVIAL
 SDITSSGAADRSQEPSPVGSRRGHVTPNLSRASSDADHGAEEDKEEQVDSQPDASSS
 QTVTPVAEPPSTEPTQPDGPTTLGPLDLLPSEELLTDTSNSSSSTGEEADLAALLPDLG
 RLLINSVFHVGAERLQQMLFSDSPFLQGFLQQCKFTDVTLSPWSGDSKCHQRRVLTyti
 PISNPLGPKSASVVETQTLFRRGPQAGGCVVDSEVLTQGIPYQDYFYTAHRYCILGLAR
 NKARLRVSSEIRYRKQPWSLVKSLIEKNSWSGIEDYFHHLERELAKAEKLSLEEGGKDA
 RGLLSGLRRRKRLPSWRAHGDGPQHDPDP CARAGIHTSGSLSSRFSEPSVDQGGGA
 GIPSALVLISIVSLIILIALNVLLFYRLWSLERTAHTFESWHSALAKGKFPQTATEWAEILA
 LQKQFHSVEVHKWRQILRASVELLDKMFSLKHLHQGITVSDPPFDTQPRPDDSFS

SEQ ID No:90 (kinectin 1 (kinesin receptor))

MEFYESAYFIVLIPSIVITVIFLFFWLFMKETLYDEVLAQKQREQKLIPTKTDKKKAEEKKN
 KKKEIQNGNLHESDSESVPDFKLSDALAVEDDQVAPVPLNVVETSSSVRERKKKEKK
 QKPVLEEQVIKESDASKIPGKKVEPVPTKQPTPPSEAAASKKKPGQKKSNGSDDQD
 KKVETLMVPSKRQEALPLHQETKQESGSGKKASSKKQKTENVFVDEPLIHATTYIPLMD
 NADSSPVVDKREVIDLLKPDQVEGIQKSGTKKLKTETDKENAEVKFKDFLLSLKTMMFSE
 DEALCVVDLLKEKSGVIQDALKKSSKGELTTLIHQLEKDKLLAAVKEDAAATKDRCKQL
 TQEMMTEKERSNVVMTRMKDRIGTLEKEHNVFQNKIHVSyQETQQMQMKFQQVREQ
 MEAEIAHLKQENGILRDAVSNTTNQLESKQSAELNKL RQDYARLVNELTEKTGKLQQUEE
 VQKKNAEQAATQLKVQLQEAERRWEEVQSYIRKRTAEHEAAQQDLQSKFVAKENEVQ
 SLHSKLTDTLVSKQQLQRLMQLMESEQKRVNKEESLQMQVQDILEQNEALKAQIQQF
 HSQIAAQTSASVLAEEHLKVIAEKDKQIKQTEDSLASERDRLTSKEEELKDIQNMNFLKA
 EVQKLQALANEQAAAAHELEKMQQSVYVKDDKIRLLEEQLQHEISNKMEEFKILNDQNK
 ALKSEVQKLQTLVSEQPNKDVVEQMEKCIQEKDEKLKTVEELLETGLIQVATKEEELNAI
 RTENSSLTKEVQDLKAKQNDQVSFASLVEELKKVIHEKDGKIKSVEELLEAEELLKVANKE
 KTVQDLKQEIKALKEEIGNVQLEKAQQLSITSKVQELQNLLKGKEEQMNTMKAVLEEKEK

DLANTGKWLQDLQEENESLKAHVQEVAQHNLKEASSASQFEELEIVLKEKGNELKRLEA
 MLKERESDLSSKTQLLQDVQDENKLFKSQIEQLKQQNYQQASSFPPHEELLKVISEREK
 EISGLWNELDLSDAVEHQKKNNDLREKNWEAMEALASTEKMLQDKVNKTSKERQQ
 QVEAVELEAKEVLKKLFPKVSVPNSLSYGEWLHGFEKKAKECMAGTSGSEEVKVLEHK
 LKEADEMHTLLQLECEKYKSVLAETEGILQKLQRSVEQEENKWVKVDESHKTIKQMQS
 SFTSSEQELERLRSENKDIENTLRREHLEMELEKAEMERSTYVTEVRELKDLLTELQK
 KLDDSYSEAVRQNEELNLLKAQLNETLTKLRTEQNERQKVAGDLHKAQQSLELIQSKIVK
 AAGDTTVIENSDVSPETESSEKETMSVSLNQTVTQLQQLQAVNQQLTKEKEHYQVLE

SEQ ID No:91 (Mesenchymal stem cell protein DSCD75)

MLGLLVALLALGLAVFALLDVWYLVRLPCAVLRARLLQPRVRDLLAEQRFPPGRVLPDDL
 DLLLHMNNARYLREADFARVAHLTRCGVLGALRELRAHTVLAASCARHRRSLRLLPEPFE
 VRTRLLGWDDRAFYLEARFVSLRDGFVCALLRFRQHLLGTSPERVVQHLCQRRVEPPE
 LPADLQHWISYNEASSQLLRMESGLSDVTKDQ

SEQ ID No:92 (Neurotrypsin)

MTLARFVLALMLGALPEVVGFDVSLNDSLHSHRHSPAPAGPHYPPYLLPTQQRPPPTTRP
 PPPLPRFPRPPRALPAQRPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLRWAE
 VPPFLERSPPASWAQLRGQRHNFCSRSPDGAGRPWCFYGDARGKVDWGYCDCRHS
 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSG
 LGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCFSHGPFTPIIRLAGGS
 SVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAHQAYFGEGSGPV
 MLDEVRCCTGNELNLSIEQCPKSSWGEHNCGHKEDAGVSCTPLTDGVIRLAGGKGSHEGR
 LEVYYRGQWGTVCDDGWTELNTYVVCRLGLGFKYQKQASANHFEESTGPIWLDDVSCS
 GKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGR
 VEVFINGQWGTICDDGWTDKDAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCT
 GNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGNSNKESSLSSVCGLRLLHRRQ
 KRIIGGKNSLRGGWPWQVSLRLKSSHGDRLLCGATLLSSCWVLTAAHCFKRYGNSTR
 SYAVRVGDYHTLVPEEFEEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSH
 VLPACLPLWRERPQKTASNCYITGWGDTGRAYSTRTLQQAAPLLPKRFCEERYKGRFT
 GRMLCAGNLHEHKRVDSCQGDGGPLMCERPGEWVVGVTWVGYGCGVKDSPGV
 YTKVSAFVPWIKSVTKL

SEQ ID No:93 (PP1, regulatory subunit 15B)

MEPGTGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPEN\$GNPTLLSSAQPE
 TRVSYWTKLLSQQLLAPLPGLLQKVLWSQLFGGMFPTRWLDFAGVYSALRALKGREKPA
 APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPDLDKLELKAKGSALDPAAQAFL
 LEQQLWGVPELLPSSLQSRLYSNRELGSSPSGPLNIQRIDDFS VVS YLLNPSYLD CFPRL E
 VSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPLSTEGLPEIH
 HLRMKRLEFLQQASKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAG
 DIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSSEIPMEKEPGEGRISVVDYSYLEG
 DLPISARPACSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSLEQ
 DPEGLHLWNSFCSDVPYNPNQFTATIQTAA RIVPEEPSDSEKDL SGKSDLENSSQSGSL
 PETPEHSSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCR
 DSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLE
 EVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQGTC
 FKGLNLVKQC

SEQ ID No:94 (Protein amplified in osteosarcoma (OS-9))

MAAETLLSSLLGLLLLGLLL PASLTGGVGS LNLEELSEMRYGIEILPLPVMGGQSQSSDV
 VIVSSKYKQRYECRLPAGAIHFQREREEETPAYQGPGIPELLSPMRDAPCLLTKDWWT
 YFCYGRHIQQYHMEDSEIKGEVLYLGYYSQAFDWDETA KASKQHRLKRYHSQTYG
 NGSKCDLNGRPREAEVRFLCDEGAGISGDYIDRVDEPLSCSYVLTIRTPRLCPHPLL RP
 PPSAAPQAILCHPSLQPEEY MAYVQRQADSKQYGDKIIEELQDLGPQVWSETKSGVAP
 QKMAGASPTKDDSKDSDFWKMLNEPEDQAPGGEEVPAEEQDPSPEAADSASGAPND
 FQNNVQVKVIRSPADLIRFIEELKGGTKKGKPNIGQE QPVDDAAEVPQREPEKERGDPE
 RQREMEEEEEDEDEDEDEDEDERQLLGEFEKELEGILLPSDRDRLRSEVKAGMERELN
 IIQETEKELDPDGLKKESERDRAMLALTSTLNKLIKRL EEKQSPELVKKHKKKRVPKPP
 PSPQPT EEDPEHRVRVRVTKLRLGGPNQDLTVLEMKREN PQLKQIEGLVKELLEREGLT
 AAGKIEIKIVRPWAEGTEEGARWLTD ETRNLKEIFFNILVPGAEEAQKERQRQKELESN
 YRRVWGSPGGEGTGDLDEFDF

SEQ ID No:95 (Protein similar to stromal cell-derived factor 2)

MAVVPLLLLGG LWSAVGASSLG VVTCGSVVKLLNTRHNVRLHSHDVR YGSGSGQQSV
 TGVTSDDSNSYWRIRGKSATVCERGTPIKCGQPIRLTHVNTGRNLHSHHFTSPLSGN
 QEVSAFGEEGEGDYLD DWTVLCNGPYWVRDGEVRFKHSSTEVL LSVTGEQYGRPI SG
 QKEVHGMAQPSQNNYWKAMEGIFMKPSELLKAEAHHAEL

SEQ ID No:96 (Protocadherin beta 8)

MEASGKLICRQRQVLFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQRE
FSRRGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLLESPFEFF
QAELQVIDINDHSPVFLDKQMLVKVSESSPPGTAFPLKNAEDLDIGQNNIENYIISPNSYF
RVLTRKRS DGRKYPELVLDNALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVVDVND
NAPEFQQPFYRVQISEDSPISFLVVKVSATDVDVTGVNGEISYSLFQASDEISKTFKVDFLT
GEIRLKKQLDFEFQSYEVNIEARDAGGFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPE
NAPETVVALFSVSDLDSENGKISCSIQEDLPFLKSSVGNFYTLLTETPLDRESRAEYN
VTITVTDLGTPRLTTHLNMTVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDR
DSGTNAQVTYSLLPPQDPHLPLASLVSINTDNHGLFALRSLDYEALQAFEFVRVGASDRG
SPALSSEALVRVLVDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDS
GQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLLSERDAAKQRLVVLVKDNGEPPCS
ATATLHLLLVDGFSQPYLPLPEAAPAQGGADSLTVYLVVALASVSSLFLFSVLLFVAVLLC
RRSRAASVGRCSVPEGPFGHLVDVRGTGSLSQNYQYEVCLAGGSGTNEFQFLKPVL
PNIQGHSGFPEMEQNSNFRNGFGFSLQLK

SEQ ID No:97 (REP8 protein)

MASRGVVGIFFLSAVPLVCLELRRGIPDIGIKDFLLLCGRILLLLALLTLIISVTTSWLNSFKS
PQVYLKEEEEKNEKRQKLVRKKQQAQGEKASRYIENVLKPHQEMKLRKLEERFYQMT
GEAWKLSSGHKLGGDEGTSQTSFETSNREAAKSQNLPKPLTEFPSPAEQPTCKEIPDL
PEEPSQTAEVVTVALRCPSGNVLRRLRFLKSYSSQVLFDWMTRIGYHISLYSLSTSFP
RPLAVEGGQSLEDIGITVDTVLILEEKEQTN

SEQ ID No:98 (RING finger protein 5)

MAAAEEEDGGPEGPNRERGGAGATFECNICLETAREAVVSVCGHLYCWPC LHQWLET
RPERQECPVCKAGISREKVPLYGRGSQKPQDPRLKTPPRPQGQRPAPESRGGFQPF
GDTGGFHFSFGVGAFPFGFFTTVFNAHEPFRRGTGVDLGQGHPASSWQDSLFLFLAIF
FFFWLLSI

SEQ ID No:99 (Retinal short-chain dehydrogenase/reductase retSDR2)

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKLV
LWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLA

YCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVN
RLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

SEQ ID No:100 (Stromal cell-derived factor 2-like 1)

MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDI
KYGSGSGQQSVTGVEASDDANSYWRIRGGSEGGCPCGSPVRCGQAVRLTHVLTGKN
LHTHHFPSPLSNNQEVSFAFGEDGEGDDLDLWTVRCSGQHWEREAAVRLQHVGTSVFL
SVTGEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

SEQ ID No:101 (Thioredoxin domain-containing protein)

GRWASGEMAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIE
FYAPWCPACQNLQPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDG
EFRRYQGPRTKKDFINFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHN
YFIEDLGLPVWGSYTVFALATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSE
SAQPLKKVEEEEQEADEEDVSEEEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

SEQ ID No:102 (Voltage-dependent anion channel 1)

AVPPTYADLGKSARDVFTKGYGFGLIKLDLKTSENGLEFTSSGSANTETTQVTGSLETK
YRWTEYGLTFTEKWNTDNTLGTEITVEDQLARGCLKLTFDSSFSPNTGKKNAKIKTGYKR
EHINLGCDMDFDIAGPSIRGALVLGYEGWLAGYQMNFFETAKSRVTQSNFAVGKYKTDEF
QLHTNVNDGTEFGGSIYQKVNKKLETAVNLAWTAGNSNTRFGIAAKYQIDPDACFSKAV
NNSSLIGLGYTQTLKPGIKLTLSALLDGKNVNAGGHKLGLGLEFQA

SEQ ID No:103 (ATP-binding cassette, sub-family A member 3)

MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFPGLIWLRLKIQSENVPNATIYPGQSI
QELPLFFTFPPPGDTWELAYIPSHSDAAKTVTETVRRALVINMRVRGFPSEKDFEDIYRY
DNCSSSVLAADVFEHPFNHSKEPLPLAVKYHLRFSYTRRNYMWTQTGSSFFLKETEGWH
TTSLFPLFPNPGPRELTSPDGGEPGYIREGFLAVQHAVDRAIMEYHADAATRQLFQRLT
VTIKRFPYPPIADPFLVAIQYQLPLLLLLSFTYALTARAVVQEKERRLKEYMRMMGLS
SWLHWSAWFLLFFLFLIAASFMTLLFCVKVKNVAVLSRSDPSLVLAFLLCFAISTISFSF
MVSTFFSKANMAAAFGGFLYFFTYIPYFFVAPRYNWMTLTSQKLCSCLLSNVAMAMGAQ
LIGKFEAKGMGIQWRDLLSPVNVDDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQF
GVPQPWYFFIMPSYWCGKPRAVAGKEEEDSDPEKALRNEYFEAEPEDLVAGIKIKHLSK
VFRVGNKDRAAVRDLNLNLYEGQITVLLGHNGAGKTTTSLMLTGLFPPTSGRAYISGYEI

SQDMVQIRKSLGLCPQHDILFDNLTVAEHLFYFAQLKGLSRQKCPEEVKQMLHIIGLEDK
WNSRSRFLSGGMRRKLSIGIALIAGSKVLILDEPTSGMDAISRRAIWDLLQRQKSDRTIVL
TTHFMDEADLLGDRIAIMAKGELQCCGSSLFLKQKYGAGYHMTLVKEPHCNPEDISQLV
HHHVPNATLESSAGAELSFILPRESTHRFEGLFAKLEKKQKELGASFGASITTMEEVFLR
VGKLVDSMDIQAIQLPALQYQHERRASDWAVDSNLCGAMDPSDGIGALIEEERTAVKL
NTGLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTALLAINYSSELFDDPM
LRLTLGEYGRTVVPFSPGTSQGLGQQLSEHLKDALQAEGQEPREVLGDLEEFIFRASV
EGGGFNERCLVAASFRDVGERTVVNALFNNQAYHSPATALAVVDNLLFKLLCGPHASIV
VSNFPQPRSAQAQKQFNEGRKGFIDIALNLLFAMAFLASTFSILAVSERAVQAKHVQF
VSGVHVASFWSALLWDLISFLIPSLLLLTVFKAQFDVRAFTRDGHMADTLLLLLLYGWAI
PLMYLMNFFFLGAATAYTRLTIFNILSGIATFLMVTIMRIPAVKLEELSKTLDHVFLVLPNH
CLGMAVSSFYENYETRTRYCTSSEVAAHYCKKYNIQYQENFYAWSAPGVGRFVASMAA
SGCAYLILLFIETNLLQRLRGILCALRRRRTLTELYTRMPVLPEDQQDVADERTRILAPSP
DSLLHTPLIIEKLSKVYEQRVPLLAVDRLSLAVQKGECFGLLGFGAGKTTTTFKMLTGEE
SLTSGDAFVGGHRISSDVGKVRQRIGYCPQFDALLDHMTGREMLVMYARLRGIPERHIG
ACVENTLRGLLLEPHANKLVRTYSGGNKRKLSTGIALIGEPVIFLDEPSTGMDPVARRL
LWDTVARARESGKAIITSHSMEECEALCTRLAIMVQGQFKCLGSPQHLKSKFGSGYSL
RAKVQSEGQQEALEEFKAFVDLTFPGSVLEDEHQGMVHYHLPGRDLSWAKVFGILEKA
KEKYGVDDYSVSQISLEQVFLSFAHLQPPTAEGR

SEQID No:104 (CAMK4)

MLKVTVPSCSASSCSVTASAAPGTASLVPDYWIDGSNRDALSDFFEVESELGRGATSI
VYRCKQKGTQKPYALKVLKKTVDKKIVRTEIGVLLRLSHPNIIKLKEIFETPTEISLVLELV
GGELFDRIVEKGYYSERDAADAVKQILEAVAYLHENGIVHRDLKPENLLYATPAPDAPLK
ADFGLSKIVEHQVLMKTVCGTPGYCAPEILRGAYGPEVDMWSVGIITYILLCGFEPFYD
ERGDQFMFRRILNCEYYFISPPWWDEVSLNAKDLVRKLIVLDPKKRLTTFQALQHPWVTG
KAANFVHMDTAQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHGSIQESHKASRDPS
PIQDGNEDMKAIPERGEKIQGDGAQAQAVKGAQAEMLKVQALEKVKGADINAEAPKMVP
KAVEDGIKVADLELEEGLAEEKLKTVEEAAAPREGQGSSAVGFEPQQDVILPEY

SEQ ID No:105 (KIAA0363)

EPCALTPGPSHLALTFLPSKPGARPQPEGASWDAGPGGAPSAWADPGEGGSPMLLP
EGLSSQALSTEAPLPATLEPRIVMGEETCQALLSPRAARTALRDQEGGHASPDPPPELC
SQGDLSVPSPPPDPDSFFTPPTPTKTTYALLPACGPHGDARDSEAELRDELLDSPPAS

PSGSYITADGDSWASSPSCSLSLAPAEGLDFPSGWGLSPQGSMVDERELHPAGTPEP
 PSSESSLADSSSSSWGQEGHFFDLDFLANDPMIPAALLPFQGSILFQVEAVEVTPLSPE
 EEEEEAVADPDPGGDLAGEGEEDSTSASFLQSLSDLSITEGMDEAFARDDTSAASSD
 SDSASYAEADDERLYSGEPHAQATLLQDSVQKTEEEESGGGAKGLQAQDGTVSWAVEA
 APQTSDRGAYLSQRQELISEVTEEGLALGQESTATVTPHTLQVAPGLQVEVATRVTQA
 GEEETDSTAGQESAAMAMPQPSQEGISEILGQESVTAEKLPPTQEETSLTLCPSQNL
 KEEGGLDLPSGRKPVAATIVPRQAKEDLTLPQDSAMTPPLPLQDQDLSSAPKPVAAATI
 VSQQAEEGLTLPQDSVMTPPLPLQDTELSSAPKPVAAATLVVSQQAEEGLTLPQDSAMT
 PPLPLQDQDLSSAPKPVAAATLVVSQQAEEGLTLPQDSAMTPPLPLQDQDLSSAPKPVAA
 ATLVVSQQAEEGLTLPQDSAMTPPLPLQDQDLSSAPKPVAAATIVVSQQAEEGLTLPQDS
 AMTPPLPLQDQDLSSAPKPVAAATIVVSQQAEEGLTLPQDSAMTPPLPLQDQDLSSAPKPV
 AAATPVVSQQAEEGLTLPQDSAMTPPLPLQDQDLSSAPKPVAAATPVVSQQAEEGLTLPQ
 DSAMTAPLPLQDGTSGPEPLAVATPQTLQAEAGCAPGTEPVATMAQQEVGEALGP
 RPAPEEKNAALPTVPEPAALDQVQQDDPQPAEAGTPWAAQEDADSTLGMEALSLPE
 PASGAGEEIAEALSRPGREACLEARAHTGDGAKPDSPQKETLEVENQQEGGLKLLAQE
 HGPRSALGGAREVPDAPPAACPEVSQARLLSPAREERGLSGKSTPEPTLPSAVATEAS
 LDSCPESSVGAVSSLDRCPCDAPAPTSAPTSQQPEPVLGLGSVEQPHEVPSVLGTPLL
 QPPENLAKGQPSTPVDRPLGPDPSAPGTLAGAALPPLEPPAPCLCQDPQEDSVEDEEP
 PGSGLGLPPPQAGVQPAAAAVSGTTQPLGTGPRVSLSPHSPLLSPKVASMDAKDLALQIL
 PPCQVPPPSGPQSPAGPQGLSAPEQQEDEDSEEDSPRALGSGQHSDSHGESSAELD
 EQDILAPQTVQCPAQAPAGGSEETIAKAKQSRSEKKARKAMSKLGLRQIQGVTRITIQKS
 KNILFVIAKPDVFKSPASDTYVVFGEAKIEDLSQQVHKAABEKFVPSEPSALVPESAPR
 PRVRLECKEEEEEEEEVDEAGLELRDIELVMAQANVSRKAVRALRDNHSDIVNAIME
 LTM

SEQID No:106 (DCTN1)

MMRQAPTARKTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLA
 APIIPTPVLTSAGVPPLPSPSKEEEGLRAQVRDLEEKLETLRKRAEDKAKLKELEKHKI
 QLEQVQEWKSKMQEQQADLQRRRLKEARKEAKEALEAKERYMEEMADTADAIEMATLD
 KEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEKGS DGAASSYQLKQLEEQNAR
 LKDALVRMRDLSSSEKQEHVKLQKLMEKKNQELEVVRQQRERLQEELSQAESTIDELK
 EQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDLEAMNEMNDELQENARETELEL
 REQLDMAGARVREAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNREL TNQQEASV
 ERQQQPPPETFDKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG

GDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYS
 LSLQATLHRYEHALSQCSVDVYKKVGSLYPEMSAHERSLDFLIELLHKDQLDET VNVE
 PLTKAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVGRLRAFLQGGQEA
 TDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQVSDTLLDCRKHLTWV
 VAVLQEVAaaaaaqliaplaenegllvaaleelafkaseqiYGTPSSSPYECLRQSCNILIS
 TMNKLATAMQEGEYDAERPPSKPPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKKS
 LKIKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLEETQALLRKKEKEFEETMDA
 LQADIDQLEAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAIPGQAP
 GSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSILKGAQMKASLASLPPLHVAKLSHEG
 PGSELPAGALYRKTSQLETLNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSD
 TVEKLKDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAG
 FGQRHRLVLTQEQLHQLHSRLIS

SEQ ID No:107 (KIAA1250)

LQLSVKMSVLISQSVINYVEEENIPALKALLEKCKDVDERNECGQTPLMIAAEQGNLEIVK
 ELIKNGANCNLEDLDNWTALISASKEGHVHIVEELLKCGVNLEHRDMGGWTALMWACY
 KGRTDVVELLLSHGANPSVTGLYSVYPIIWAAGRGHADIVHLLLQNGAKVNCSDKYGTT
 PLVWAARKGHLECVKHLLAMGADV DQEGANSMTALIVAVKGGYTQSVKEILKRNPVN
 LTDKDGN TALMIASKEGHT EIVQDLLDAGTYVNIPDRSGDTV LIGAVRGGHVEIVRALLQ
 KYADIDIRGQDNKTALYWAVEKGNATMVRDILQCNPDTEICTKDGETPLIKATKMRNIEV
 VELLDDKGAKVSAVDKKGDTPLHIAIRGRSRKLAELLRNPKDGRLLYRPNKAGETPYNI
 DCSHQKSILTQIFGARHLSPTETDGDMLGYDLYSSALADILSEPTMQPPICVGLYAQWG
 SGKSFLLKKLEDEMKT FAGQQIEPLFQFSWLIVFLTLLCGGLGLLFAFTVHPNLGIAVSL
 SFLALLYIFFIVIYFGGRREGESWNWAWVLSTRLARHIGYLELLLKLMFVNPPPELPEQTTK
 ALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREFGLATRLFRVFKTEDTQGKKK
 WKKTCCLPSFVIFLFIIGCIISGITLLAIFRVDPKHLTVNAVLSIASVVG LAFVLNCR TWWQ
 VLDSLLNSQRKRLHNAASKLHKLKSEGFMKVLKCEVELMARMAKTIDSFTQNQTRLVVII
 DGLDACEQDKVLQMLDTVRVLFSGKPFIAIFASDPHIIKAINQNLNSVLRDSNINGHDYM
 RNIVHLPVFLNSRGLSNARKFLVTSATNGDVPCSDTTGIQEDADRRVSQNSLGEMTKLG
 SKTALNRRDTYRRRQMQR TITRQMSFDLTKLLVTE DWFS DISPQTMRRLNIVSVTGR L
 LRANQISFNWDR LASWINLTEQWPYRTSWLILYLEETEGIPDQMTLKT IYERISKNIPTTK
 DVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKVFLPCTVNLDPKLREI IADVRAAREQISIG
 GLAYPPLPLHEGPPRAPSGYSQPPSVCSSTSFNGPFAGGVVSPQPHSSYYSGMTGPQ
 HPFYNRPF FAPYLYTPRYYPGGSQHLISRPSVKTS LPRDQNNGLEVIKEDAAEGLSSPT

DSSRGSGPAPGPVLLNSLNVDACEKLKQIEGLDQSMLPQYCTTIKKANINGRVLAQC
 NIDELKKEMNMNFGDWHLFRSTVLEMRNAESHVVPEDPRFLSESSSGPAPHGEPARR
 ASHNELPHTELSSQTPYTLNFSFEELNTLGLDEGAPRHSNLSWQSQTRRTPSLSSLNS
 QDSSIEISKLTDKVQAEYRDAYREYIAQMSQLEGGPGSTTISGRSSPHSTYYMGQSSSG
 GSIHSNLEQEKGKDSEPKPDDGRKSFLMKRGDVIDYSSSGVSTNDASPLDPITEEDEKS
 DQSGSKLLPGKKSSERSSLFQTDLKLKGSGLRYQKLPSDEDESGTEESDNTPLLKDDK
 DRKAEGKVERVPKSPEHSAEPIRTFIKAKEYLSDALDKKDSSDSGVRSSSESSPNHSLH
 NEVADDSQLEKANLIELEDDSHSGKRGIPHSLSGLQDPPIARMSICSEDKKSPSECSLIAS
 SPEENWPACQKAYNLNRTPTSTVTLNNNSAPANRANQNFDMEGIRETSQVILRPSSSP
 NPTTIQENENLKSMTHKRSQRSSYTRLKDPPELHAAASSESTGFGEERESIL

SEQID No:108 (FACL3)

MNNHVSSKPSTMKLKHTINPILLYFIHFLISLYTILTYIPFYFFSESRQEKSNNRIKAKPVNSK
 PDSAYRSVNSLDGLASVLYPGCDTLDKVFTYAKNKFKNKRLLGTREVLNEEDEVPNG
 KIFKKVILGQYNWLSYEDVFVRAFNFNGNLQMLGQPKTNIAIFCETRAEWMIAAQACF
 MYNFQLVTLYATLGGAIVHALNETEVTNIITSKELLQTKLKDIVSLVPRLRHITVDGKPPT
 WSDFPKGIIVHTMAAVEALGAKASMENQPHSKPLPSDIAVIMYTSGSTGLPKGVMISHS
 NIIAGITGMAERIPELGEEDVYIGYLPLAHVLELSAELVCLSHGCRIGYSSPQTLADQSSKI
 KKGSKGDTSMKPTLMAAVPEIMDRIYKNVMNKVSEMSSFQRNLFILAYNYKMEQISKG
 RNTPLCDSFVFRKVRSLGGINRLLLCGGAPLSATTQRFMNICFCCPVGGQGYGLTESAG
 AGTISEVWDYNTGRVGAPLVCCEIKLKNWEEGGYFNTDKPHPRGEILIGGQSVTMGY
 KNEAKTKADFSEDENGQRWLCTGDIGEFEPDGCLKIIDRKKDLVKLQAGEYVSLGKVEA
 ALKNLPLVDNICAYANSYHSYVIGFVVPNQKELTELARKKGLKGTWEELCNCEMENEV
 LKVLSEAAISASLEKFEIPVKIRLSPEPWTPETGLVTDFAFKLKRKELKTHYQADIERMYGR
 K

SEQID No:109 (FACL4)

MKLKLNVLTIILLPVHLLITIYSALIFIPWYFLTNAKKKNAMAKRIKAKPTSDKPGSPYRSVT
 HFDSLAVIDIPGADTLDKLFDAVSKFGKKDSLGTREILSEENEMQPNGKVFKKLILGNY
 KWMNYLEVNRVNNFGSGLTALGLKPKNTIAIFCETRAEWMIAAQTCFKYNFPLVTLYA
 TLGKEAVVHGLNESEASYLITSVELLESKLKTALLDISCVKHIIYVDNKAINKAEYPEGFEIH
 SMQSVEELGSPENLGIPPSRPTPSDMAIVMYTSGSTGRPKGVMHHSNLIAGMTGQC
 ERIPGLGPKDITYIGYLPLAHVLELTAEISCFTYGCGRIGYSSPLTSDQSSKIKKGSKGDCT
 VLKPTLMAAVPEIMDRIYKNVMSKVQEMNYIQKTLFKIGYDYKLEQIKKGYDAPLCNLLLF

KKVKALLGGNVRMMLSGGAPLSPQTHRFMNVCFCPIGQGYGLTESCGAGTVTEVTD
 YTTGRVGAPLICCEIKLDWQEGGYTINDKPNPRGEIVIGGQNISMGYFKNEEKTAEDYS
 VDENGQRWFCTGDIGEFHPDGCLQIIDRKKDLVKLQAGEYVSLGKVEAALKNCPLIDNIC
 AFAKSDQSYVISFVVPNQKRLTLLAQKQGVGTWVDICNNPAMEAEILKEIREAANAMKL
 ERFEIPIKVRLSPEPWTPETGLVTDAFKLKRKELRNHYLKDIERMYGGK

SEQID No:110 (KIAA0095)

MDTEGFGELLQQAELAAETEGISELPHVERNLOEIQQAGERLRSRTLTRTSQETADV
 ASVLLGSRGLDISHISQRLESLSAATTFEPLPVKDTDIQGFLKNEKDNALLSAIEESRKR
 TFGMAEEYHRESMLVEWEQVKQRILHTLLASGEDALDFTQESEPSYISDVGPPGRSSL
 DNIEMAYARQIYIYNEKIVNGHLQPNLVDLCASVAELDDKSISDMWTMVKQMTDVLTPA
 TDALKNRSSVEVRMEFVRQALAYLEQSYKNYTLVTVFGNLHQAQLGGVPGTYQLVRSF
 LNIKLPAPLPGLQDGEVEGHPVWALIYYCMRCGDLLAASQVVNRAQHQLGEFKTWFAQE
 YMNSKDRRLSPATENKLRLHYRRALRNNTDPYKRAVYCIIGRCDVTDNQSEVADKTED
 YLWLKLNQVCFDDDGTSPPQDRLTSLQFQKQLLEDYGESHTVNVQPPFLYFQVFLTA
 QFEAAVAFLFRMERLRCHAVHVALVLFELKLLKSSGQSAQLLSHEPGDPPCLRRLNFV
 RLLMLYTRKFESTDPREALQYFYFLRDEKDSQGENMFLRCVSELVIESREFDMILGKLE
 NDGSRKPGVIDKFTSDTKPIINKVASVAENKGLFEEAAKLYDLAKNADKVELELMNKLLSP
 VVPQISAPQSNKERLKNMALSIAERYRAQGISANKFVDSTFYLLDLITFFDEYHSGHIDR
 AFDIERLKLVLPLNQESVEERVAEFRNFSDEIRHNLSEVLLATMNILFTQFKRLKGTSPSS
 SSRPQRVIEDRDSQLRSQARTLITFAGMIPYRTSGDTNARLVQMEVLMN

SEQID No:111 (KIAA0922)

MLLVLECVLFSVAQGYFRMDSSATQFHIETHENTSGLWSIWYRNHFDRSVVLNDVFLSK
 ETKHMLKILNFTGPLFLPPGCWNIFSLKLAVKDIAINLFTNVFLTTNIGAIFAIPLQIYSAPTK
 EGS LGFEVIAHCGMHYFMGKSKAGNPWNWNGSLSLDQSTWNVDSELANKLYERWKKYK
 NGDVCKRNVLGTTTRFAHLKKSKESESFVFFLPRLIAEPGLMLNFSATALRSRMIKYFVVQ
 NPSSWPVSLQLLPLSLYPKPEALVHLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSE
 ESRFGILHLHLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFGARELLKVG
 GRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSITKNFKVENIGPLPITVSSLKINGYNC
 QGYGFEVLDCHQFSLDPNTSRDISIVFTPDTSSWVIRDLSLVTAADLEFRFTLNVTLPH
 HLLPLCADVVPGPSWEESFWRLTVFFVSLSLGVLIAFQQAQYILMEFMKTRQRQNAS
 SSSQQNNGPMDVISPHSYKSNCKNFLDTYGPSDKGRGKNCLPVNTPQSRIQNAAKRSP
 ATYGHSQKKHKCSVYYSKHKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRE

NWISLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECSMKEGIQTCMFPKE
 TDIKTSSENTAEFKERELCPLKTSKKLPENHLPRNSPQYHQPDLPESISRKNNNGNNQQVPV
 KNEVDHCENLKKVDTKPSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREG
 NLQNLNWSKSRCTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELSSDINVRSWCIQE
 STREVCKADAEIASSLPAAQREAEGYYQKPEKKCVDKFCSDSSSDCGSSSGSVRASRG
 SWGWSWSSTSSSDGDKKPMVDAQHFLPAGDSVSQNDPSEAPISLNLSHNICNPMTVN
 SLPQYAEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLENGVPCVIQE
 SAPVHNSFIDWSATCEGQFSSAYCPELNDYNAFPEENMNYANGFPCPADVQTDIDH
 NSQSTWNTPPNMPAAWGHASFISSPPYLTSTRSLSPMSGLFGSIWAPQSDVYENCPI
 NPTTEHSTHMENQAVVCKEYYPGFNPFRAVMNLDIWTTTANRANFPLSRDSSYCGNV

SEQ ID No:112 (PAS domain containing serine/threonine kinase)

MEDGGLTAFEEDQRCLSQSLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLC
 QSRTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSS
 GWSSPLLPAVPCNPKNKAIFTVDAKTTEILVANDKACGLLYSSQDLIGQKLTQFFLRSDS
 DVVEALSEEHMEADGHAHVFGTVVDIISRSGEKIPVSVWMKRMQRERRLCCVVVLEP
 VERVSTWVAFQSDGTVTSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIPKN
 LKIQRSVGRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLP
 DGTIHGINHSFALTIFGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNE
 SGCGERTLDPWQGQDPAEGGQDPRINVVLGGHVPRDEIRKLMEQDIFTGTQTELI
 AGGQLLSCLSPQPAPGVDNVPEGSLPVHGEQALPKDQQITALGREEPVAIESPGQDLL
 GESRSEPVDVKPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDL
 WAGAAVAKPQAKGQLAGGSLLMHCPCYGSEWGLWWRSQDLAPSPSGMAGLSFGTP
 TLDEPWLGVENDREELQTCLIKEQLSQLSLAGALDVPHAELVPTECQAVTAPVSSCDLG
 GRDLCGGCTGSSSACYALATDLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSS
 NCSCATSELRETPSSLAVGSDPDVGSQEQGSCVLDDRELLLLTGTCVDLGQGRRFRE
 SCVGHDPTPELEVCLVSSEHYAASDRESPGHVPSTLDAGPEDTCPSAEERPRLNVQVTS
 TPVIVMRGAAGLQREIQEGAYSGSCHHRDGLRLSIQFEVRRVELQGPTPLFCCWLVKDL
 LHSQRDSAARTRLFLASLPGSTHSTAELTGPSLVEVLRARPWFEEPPKAVELEGLAAC
 EGEYSQKYSTMSPLGSGAFGFVWTAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLGKV
 TLEIAILSRVEHANIIVLDIFENQGGFFQLVMEKHGSGLDLFAFIDRHPRLDEPLASYIFRQL
 VSAVGYLRLKDIIHRDIKDENVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLM
 GNPYRGPELEMWSLGVTLTYTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQP

VPERRTTLEKLVTDPWVTQPVNLADYTWEEVCRVNKPESGVLSAASLEMGNRSLSDVA
QAQELCGGPVPGAPNGQGCLHPGDPRLTS

SEQID No:114 (homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)
HPAGLAAAAAGTPRLPSKRRIPVSQPGMADPHQLFDDTSSAQSRGYGAQRAPGGLSY
PAASPTPHAAFLADPVSNMAMAYGSSLAQAQKELVDKNIDRFIPITKLKYFAVDTMVVG
RKLGLLFFPYLHQDWEVQYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDR
FSPDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFLGYKYVGMIGGVLMGL
LFGKIGYYLVLGWCCVAIFVFMIRTLRLKILADAAAEGVPVRGARNQLRMYLTMAVAAAQ
PMLMYWLTFHLVR

SEQ ID No:114 (Integral membrane transporter protein)

MVNYAWAGRSQRKLWWSVAVLTCKSVVRPGYRGGLQARRSTLLKTCARARATAPG
AMKMVAPWTRFYNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFSSE
LGGDFEFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAIT
VLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYLISCVWNCYRYING
RNSSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA

SEQID No:115 (GPR49)

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDLGLS
ELPSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYPKGAFGLYSLKVL
MLQNNQLRHVPTEALQNLRLSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIP
VQAFRSLSALQAMTLALNKHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLETL
DLNYYNNLDEFPTAIRTLNKLKELGFHSNNIRSIPEKAFVGNPSLTIHFYDNPIQFVGRSAF
QHLPELRTLTLNGASQITEFPDLTGANLESLTLTGAQISSLPQTVCNQLPNLQVLDLSY
NLLEDLPFSFVCQKLQKIDLRHNEIYEIKVDTFQQLSLRSLNLAWNKIAIHPNAFSTLPS
LIKLDLSSNLLSSFPITGLHGLTHLKLGTGNHALQSLISSENFPELKVIEMPYAYQCCAFGV
CENAYKISNQWNKGDNSSMDDLHKKDAGMFAQQDERDLEDFLDFFEDLKALHSVQC
SPSPGPFKPCHELLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVN
MLTGVSASVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALER
GFSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPTM
GYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCPVAF
LSFSSLINLTFISPEVIKIFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHP
SLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPC

SEQ ID No:116 (NAP-1 related protein/NAP-1-like protein)

KEQSELDQDLDDVEEVEEEETGEETKLKARQLTVQMMQNPQILAALQERLDGLVETPT
GYIESLPRVVKRRVNALKNLQVKCAQIEAKFYEEVHDLERKYAVLYQPLFDKRFEIINAIY
EPTEEEC EWKPDEEDEISEELKEKAKIEDEKKDEEKEDPKGIPEFWLTVFKNVDLLSDM
VQEHDEPILKHLKDIKVKFSDAGQPMSFVLEFHFEPNEYFTNEVLTKTYRMRSEPDDSD
PFSFDGPEIMGCTGCQIDWKKGKNVTLKTIKKKQKHKGRTVTVTKTVSND SFFNFFA
PPEVIPKFSAFDDDAEAILAADFEIGHFLRERIIPRSVLYFTGEAIEDDDDDYDEEGEEAD
EGYQLFE EVKSCSKLFQRWLQ

SEQID No:117 (SPTLC2)

MRPEPGGCCCRRTVRANGCVANGEVRNGYVRSSAAAAAAAAAAGQIHHTVQNGGLYK
RPFNEAFEETPMLVAVLTYVGYGVLT LFGYLRDFLRYWRIEKCHHATEREEQKDFVSLY
QDFENFYTRNLYMRIRDNWNRPICSVPGARVDIMERQSHDYNWSFKYTGNIIKGVINMG
SYNYLGFARNTGSCQEAAAKVLEEY GAGVCSTRQEIGNLDKHEELEELVARFLGVEAA
MAYGMGFATNSMNIPALVGKGCLILSDELNHASLVLGARLSGATIRIFKHNNMQSLEKLL
KDAIVYGQPRTRRPWKILILVEGIYSMEGSIVRLPEVIALKKKYKAYLYLDEAHSIGALGP
TGRGVVEYFGLDPEDVDVMMGTFTKSFGASGGYIGGKKELIDYLRTHSHSAVYATSLSP
PVVEQIITSMK CIMGQDGTSLGKECVQQLAENTRYFRRRLKEMGFIIYGNE DSPVPLML
YMPAKIGAFGREMLKRNIGVVVVGFPATPIESRARFCLSAHTKEILD TALKEIDEVGDLL
QLKYSRHRLVPLLD RPFDETTYEETD

SEQID No:118 (Delta-like homolog)

MTATEALLRVLLLLLAFGHSTYGAECFPACNPQNGFCEDDNVCRCQPGWQG PLCDQC
VTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRACSSAPCANNGTCVSLDGGGLYECS
CAPGYSGKDCQKKDGPCVINGSPCQHGGTCVDDEGRASHASCLCPPGFSGNFCEIVA
NSCTPNPCENDGVCTDIGGDFRCRCPAGFIDKTC SRPVTNCASSPCQNGGTCLQHTQ
VSYECLCKPEFTGLTCVKKRALSPQQVTRLPSGYGLAYRLTPGVHEL PVQQPEHRILKV
SMKELNKKTPLLTEGQAICFTILGVLTSLVVLGTVGIVFLNKCETWVSNLRYNHMLRKKK
NLLLQYNSGEDLAVNIIFPEKIDMTTFSKEAGDEEI

SEQ ID No: 119 (25 kDa microsomal signal peptidase subunit)

MAAAAVQGGRSGSGGCSGAGGASNCGTGSGRSGLLDKWKIDDKPVKIDKWDGSAV
KNSLDDSAKKVLEKYKYVENFGLIDGRLTICTISCF FAIVALIWDYMHPPESKPVLALCV

ISYFVMMGILTIYTSYKEKSIFLVAHRKDPTGMDPDDIWQLSSSLKRFDDKYTLKLTFISG
RTKQQREAEFTKSIKFFDHSGTLVMDAYEPEISRLHDSLAIERKIK

SEQ ID No: 120 (APP-C99)

MDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSI
HHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN

SEQ ID No: 121 (Psen-2)

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDG
EEDPDRYVCSGVPGRPPGLEEELTKYGAKHVIMLFVPVTLCMIVVATIKSVRFYTEKN
GQLIYTPFTEDTPSVGQRLNLSVLNLTLMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLM
LLFLFTYIYLGEVLKTYNVAMDYPTLLLTWVNFAGVGMVCIHWKGPLVLQQAYLIMISAL
MALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALYSSAMV
WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEE
ERGVKLGGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPI
SITFGLIFYFSTDNLVRPFMDTLASHQLYI

SEQ ID No: 122 (FADS1)

MGTRAARPAG LPCGAENPAR RRLALGARQQ IHSWSPRTPS TRLTAPAGPA
RGVARPAMAP DPVAAETAAQ GPTPRYFTWD EVAQRSGCEE RWLVIDRKVY
NISEFTRRHP GGSRVISHYA GQDATDPFVA FHINKGLVKK YMNSLLIGEL
SPEQPSLEPT KNKELTDEFR ELRATVERMG LMKANHVFFL LYLLHILLE
GAAWLTLWVF GTSFLPFLC AVLLSAVQAQ AGWLQHDFFGH LSVFSTSKWN
HLLHHFVIGH LKGAPASWWS HMHFQHHAKP NCFRKDPDIN MHPFFFALGK
ILSVELGKQK KKYMPYNHGH KYFFLIGPPA LLPLYFQWYI FYFVIQRKKW
VDLAWMITFY VRFFLTYPVPL LGLKAFLGLF FIVRFLESNW FWVVTQMNHI
PMHIDHDRNM DWVSTQLQAT CNVHKSAFND WFSGHLNFQI EHHLFPTMPR
HNYHKVAPLV QSLCAKHGIE YQSKPLLSAF ADIIHSLKES GQLWLDAYLH Q

SEQ ID No: 123 (DEGS)

MGSRVSREDF EWVYTDQPHA DRRREILAKY PEIKSLMKPD PNLIWIIIMM
VLTQLGAFYI VKDLWKWVI FGAYAFGSCI NHSMTLAIHE IAHNAAFGNC
KAMWNRWFGM FANLPIGIPY SISFKRYHMD HHRYLGADGV DVDIPTDFEG
WFFCTAFRKF IWVILQPLFY AFRPLFINPK PITYLEVINT VAQVTFDILI YYFLGIKSLV

YMLAASLLGL GLHPISGHFI AEHYMFLKGH ETYSYYGPLN LLTFNVGYHN
EHHDFPNIPG KSLPLVRKIA AEYYDNLPHY NSWIKVLYDF VMDDTISPYS
RMKRHQKGEM VLE

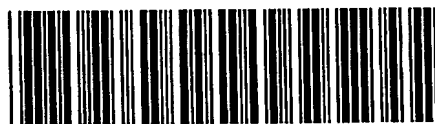
SEQ ID No: 124 (SCD4/ HYPOTHETICAL PROTEIN FLJ21032)

MPGPATDAGK IPFCDAKEEI RAGLESSEGG GGPERPGARG QRQNIVWRNV
VLMSLLHLGA VYSLVLIPKA KPLTLLWAYF CLLAALGVT AGAHLRLWSHR
SYRAKLPLRI FLAVANSMAF QNDIFERSRD HRAHHKYSET DADPHNARRG
FFFSHIGWLF VRKHRDVIEK GRKLDVTDLL ADPVVRIQRN TQHIQKEGRA
LNQEAACEML REWHQGHILK VTLPLGLHILA LLHTHCNHSE KCCLMLRALS VSLEVF

SEQ ID No: 125 (FADS3)

MGGVGEPGPR EGPAQPGAPL PTFCWEQIRA HDQPGDKWLV IERRVYDISR
WAQRHPGGSR LIGHHGAEDA TDAFRAFHQD LNFVRKFLQP LLIGELAPEE
PSQDGPLNAQ LVEDFRALHQ AAEDMKLFDA SPTFFAFLLG HILAMEVLAW
LLIYLLGPGW VPSALAAFIL AISQAQSWCL QHDLGHASIF KKSWWNHVAQ
KFVMGQLKGF SAHWWNFRHF QHHAKPNIFH KDPDVTVPV FLLGESSVEY
GKKKRRLPY NQQHLYFFLI GPPLTLVNF EVENLAYMLV CMQWADLLWA
ASFYARFFLS YLPFYGVPGV LLFFVAVRVL ESHWFVWITQ MNHIPKEIGH
EKHRDWVSSQ LAATCNVEPS LFTNWFSGHL NFQIEHHLFP RMPRHNYSRV
APLVKSLCAK HGLSYEVKPF LTALVDIVRS LKKSGDIWLD AYLHQ

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